

12-10-01

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Schulein, Martin
Andersen, Lene N.
Lassen, Soren F.
Kauppinen, Markus S.
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Ihara, Michiko
Takagi, Shinobu

(ii) TITLE OF INVENTION: Novel Endoglucanases

(iii) NUMBER OF SEQUENCES: 109

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Novo Nordisk of North America, Inc.
(B) STREET: 405 Lexington Avenue, 64th Floor
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States of America
(F) ZIP: 10174-6401

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 10/007,521
(B) FILING DATE: 10 December 2001
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Lambiris, Elias J.
(B) REGISTRATION NUMBER: 33,728
(C) REFERENCE/DOCKET NUMBER: 4366.200-US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 212-867-0123
(B) TELEFAX: 212-878-9655

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 960 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 113..787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAGAAAGGC TCTCTGCTGT CGTCGCTCTC GTCGCTCTCG TCGGCATCCT CCATCCGTCC	60		
GCCTTGATA ACCCGCTCCC CGACTCAGTC AAGACGACGC ATACTTGGCA CC ATG	115		
Met			
1			
CAT CTC TCC GCC ACC ACC GGG TTC CTC GCC CTC CCG GTC CTG GCC CTG	163		
His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala Leu			
5	10	15	
GAC CAG CTC TCG GGC ATC GGC CAG ACG ACC CGG TAC TGG GAC TGC TGC	211		
Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys Cys			
20	25	30	
AAG CCG AGC TGC GCC TGG CCC GGC AAG GGC CCC TCG TCT CCG GTG CAG	259		
Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val Gln			
35	40	45	
GCC TGC GAC AAG AAC GAC AAC CCG CTC AAC GAC GGC GGC TCC ACC CGG	307		
Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr Arg			
50	55	60	65
TCC GGC TGC GAC GCG GGC AGC GGC TAC ATG TGC TCC TCC CAG AGC	355		
Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln Ser			
70	75	80	
CCC TGG GCC GTC AGC GAC GAG CTG TCG TAC GGC TGG GCG GCC GTC AAG	403		
Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val Lys			
85	90	95	
CTC GCC GGC AGC TCC GAG TCG CAG TGG TGC TGC GCC TGC TAC GAG CTG	451		
Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu Leu			
100	105	110	
ACC TTC ACC AGC GGG CCG GTC GCG GGC AAG AAG ATG ATT GTG CAG GCG	499		
Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln Ala			
115	120	125	
ACC AAC ACC GGT GGC GAC CTG GGC GAC AAC CAC TTT GAC CTG GCC ATC	547		
Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala Ile			
130	135	140	145
CCC GGT GGC GGT GTC ATT TTC AAC GGC TGC ACC GAC CAG TAC GGC	595		
Pro Gly Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr Gly			
150	155	160	
GCT CCC CCG AAC GGC TGG GGC GAC CGC TAC GGC GGC ATC CAT TCC AAG	643		
Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser Lys			
165	170	175	

GAA GAG TGC GAA TCC TTC CCG GAG GCC CTC AAG CCC GGC TGC AAC TGG	691
Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn Trp	
180 185 190	
CGC TTC GAC TGG TTC CAA AAC GCC GAC AAC CCG TCG GTC ACC TTC CAG	739
Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe Gln	
195 200 205	
GAG GTG GCC TGC CCG TCG GAG CTC ACG TCC AAG AGC GGC TGC TCC CGT	7877
Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser Arg	
210 215 220 225	
TAAGAGGGAA GAGAGGGGGC TGGAAGGACC GAAAGATTCA ACCTCTGCTC CTGCTGGGGA	847
AGCTCGGGCG CGAGTGTGAA ACTGGTGTAA ATATTGTGGC ACACACAAGC TACTACAGTC	907
CGTCTGCCG TCCGGCTAAC TAGCCTTGCT GCGGATCTGT CCAAAAAAAA AAA	960

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 225 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala
1 5 10 15

Leu Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys
20 25 30

Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val
35 40 45

Gln Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr
50 55 60

Arg Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln
 65 70 75 80

Ser Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val
85 90 95

Lys Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu
 100 105 110

Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln
115 120 125

Ala Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala
130 135 140

Ile Pro Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr
145 150 155 160

Gly Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser
165 170 175

Lys Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn
180 185 190

Trp Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe
195 200 205

Gln Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser
210 215 220

Arg
225

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 894 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG CAT CTC TCC GCC ACC ACC GGG TTC CTC GCC CTC CCG GTC CTG GCC 48
Met His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala
230 235 240

CTG GAC CAG CTC TCG GGC ATC GGC CAG ACG ACC CGG TAC TGG GAC TGC 96
Leu Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys
245 250 255

TGC AAG CCG AGC TGC GCC TGG CCC GGC AAG GGC CCC TCG TCT CCG GTG 144
Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val
260 265 270

CAG GCC TGC GAC AAG AAC GAC AAC CCG CTC AAC GAC GGC GGC TCC ACC 192
Gln Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr
275 280 285

CGG TCC GGC TGC GAC GCG GGC AGC GCC TAC ATG TGC TCC TCC CAG 240
Arg Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln
290 295 300 305

AGC CCC TGG GCC GTC AGC GAC GAG CTG TCG TAC GGC TGG GCG GCC GTC		288	
Ser Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val			
310	315	320	
AAG CTC GCC GGC AGC TCC GAG TCG CAG TGG TGC TGC GCC TGC TAC GAG		336	
Lys Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu			
325	330	335	
CTG ACC TTC ACC AGC GGG CCG GTC GCG GGC AAG AAG ATG ATT GTG CAG		384	
Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln			
340	345	350	
GCG ACC AAC ACC GGT GGC GAC CTG GGC GAC AAC CAC TTT GAC CTG GCC		432	
Ala Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala			
355	360	365	
ATC CCC GGT GGC GGT GTC GGT ATT TTC AAC GCC TGC ACC GAC CAG TAC		480	
Ile Pro Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr			
370	375	380	385
GGC GCT CCC CCG AAC GGC TGG GGC GAC CGC TAC GGC GGC ATC CAT TCC		528	
Gly Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser			
390	395	400	
AAG GAA GAG TGC GAA TCC TTC CCG GAG GCC CTC AAG CCC GGC TGC AAC		576	
Lys Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn			
405	410	415	
TGG CGC TTC GAC TGG TTC CAA AAC GCC GAC AAC CCG TCG GTC ACC TTC		624	
Trp Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe			
420	425	430	
CAG GAG GTG GCC TGC CCG TCG GAG CTC ACG TCC AAG AGC GGC TGC TCC		672	
Gln Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser			
435	440	445	
CGT CCC TCC AGC AGC ACC AGC TCT CCG GTC AAC CAG CCT ACC AGC ACC		720	
Arg Pro Ser Ser Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr			
450	455	460	465
AGC ACC ACG TCC ACC TCC ACC ACC TCG AGC CCG CCA GTC CAG CCT ACG		768	
Ser Thr Thr Ser Thr Ser Thr Ser Ser Pro Pro Val Gln Pro Thr			
470	475	480	
ACT CCC AGC GGC TGC ACT GCT GAG AGG TGG GCT CAG TGC GGC GGC AAT		816	
Thr Pro Ser Gly Cys Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn			
485	490	495	
GGC TGG AGC GGC TGC ACC ACC TGC GTC GCT GGC AGC ACT TGC ACG AAG		864	
Gly Trp Ser Gly Cys Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys			
500	505	510	
ATT AAT GAC TGG TAC CAT CAG TGC CTG TAG		894	
Ile Asn Asp Trp Tyr His Gln Cys Leu			
515	520		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala
1 5 10 15

Leu Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys
20 25 30

Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val
35 40 45

Gln Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr
50 55 60

Arg Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln
65 70 75 80

Ser Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val
85 90 95

Lys Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu
100 105 110

Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Met Ile Val Gln
115 120 125

Ala Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala
130 135 140

Ile Pro Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr
145 150 155 160

Gly Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser
165 170 175

Lys Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn
180 185 190

Trp Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe
195 200 205

Gln Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser
210 215 220

Arg Pro Ser Ser Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr
225 230 235 240

Ser Thr Thr Ser Thr Thr Ser Ser Pro Pro Val Gln Pro Thr
 245 250 255
 Thr Pro Ser Gly Cys Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn
 260 265 270
 Gly Trp Ser Gly Cys Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys
 275 280 285
 Ile Asn Asp Trp Tyr His Gln Cys Leu
 290 295

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 927 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG CAT CTC TCC GCC ACC ACC GGG TTC CTC GCC CTC CCG GTC CTG GCC	48
Met His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala	
300 305 310	
CTG GAC CAG CTC TCG GGC ATC GGC CAG ACG ACC CGG TAC TGG GAC TGC	96
Leu Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys	
315 320 325	
TGC AAG CCG AGC TGC GCC TGG CCC GGC AAG GGC CCC TCG TCT CCG GTG	144
Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val	
330 335 340 345	
CAG GCC TGC GAC AAG AAC GAC AAC CCG CTC AAC GAC GGC GGC TCC ACC	192
Gln Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Ser Thr	
350 355 360	
CGG TCC GGC TGC GAC GCG GGC AGC GCC TAC ATG TGC TCC TCC CAG	240
Arg Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln	
365 370 375	
AGC CCC TGG GCC GTC AGC GAC GAG CTG TCG TAC GGC TGG GCG GGC GTC	288
Ser Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val	
380 385 390	
AAG CTC GCC GGC AGC TCC GAG TCG CAG TGG TGC TGC GCC TAC GAG	336
Lys Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu	
395 400 405	

CTG ACC TTC ACC AGC GGG CCG GTC GCG GGC AAG AAG ATG ATT GTG CAG	384
Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln	
410 415 420 425	
GCG ACC AAC ACC GGT GGC GAC CTG GGC GAC AAC CAC TTT GAC CTG GCC	432
Ala Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala	
· 430 435 440	
ATC CCC GGT GGC GGT GTC GGT ATT TTC AAC GCC TGC ACC GAC CAG TAC	480
Ile Pro Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr	
445 450 455	
GGC GCT CCC CCG AAC GGC TGG GGC GAC CGC TAC GGC GGC ATC CAT TCC	528
Gly Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser	
460 465 470	
AAG GAA GAG TGC GAA TCC TTC CCG GAG GCC CTC AAG CCC GGC TGC AAC	576
Lys Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn	
475 480 485	
TGG CGC TTC GAC TGG TTC CAA AAC GCC GAC AAC CCG TCG GTC ACC TTC	624
Trp Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe	
490 495 500 505	
CAG GAG GTG GCC TGC CCG TCG GAG CTC ACG TCC AAG AGC GGC TGC TCC	672
Gln Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser	
510 515 520	
CGT AAC GAC GAC GGC AAC TTC CCT GCC GTC CAG ATC CCC TCC AGC AGC	720
Arg Asn Asp Asp Gly Asn Phe Pro Ala Val Gln Ile Pro Ser Ser Ser	
525 530 535	
ACC AGC TCT CCG GTC AAC CAG CCT ACC AGC ACC AGC ACC ACG TCC ACC	768
Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr Ser Thr Thr Ser Thr	
540 545 550	
TCC ACC ACC TCG AGC CCG CCA GTC CAG CCT ACG ACT CCC AGC GGC TGC	816
Ser Thr Thr Ser Ser Pro Pro Val Gln Pro Thr Thr Pro Ser Gly Cys	
555 560 565	
ACT GCT GAG AGG TGG GCT CAG TGC GGC GGC AAT GGC TGG AGC GGC TGC	864
Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn Gly Trp Ser Gly Cys	
570 575 580 585	
ACC ACC TGC GTC GCT GGC AGC ACT TGC ACG AAG ATT AAT GAC TGG TAC	912
Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys Ile Asn Asp Trp Tyr	
590 595 600	
CAT CAG TGC CTG TAG	927
His Gln Cys Leu	
605	

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala
1 5 10 15

Leu Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys
20 25 30

Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val
35 40 45

Gln Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr
50 55 60

Arg Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln
65 70 75 80

Ser Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val
85 90 95

Lys Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu
100 105 110

Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln
115 120 125

Ala Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala
130 135 140

Ile Pro Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr
145 150 155 160

Gly Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser
165 170 175

Lys Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn
180 185 190

Trp Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe
195 200 205

Gln Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser
210 215 220

Arg Asn Asp Asp Gly Asn Phe Pro Ala Val Gln Ile Pro Ser Ser Ser
225 230 235 240

Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr Ser Thr Ser Thr
245 250 255

Ser Thr Thr Ser Ser Pro Pro Val Gln Pro Thr Thr Pro Ser Gly Cys
260 265 270

Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn Gly Trp Ser Gly Cys
275 280 285

Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys Ile Asn Asp Trp Tyr
290 295 300

His_Gln_Cys_Leu
305

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 51..935
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCAGTGTGCT GGAAAGCCTT CGTGCTGTCC CCGACGTATC CCTGACCGCC ATG CGT	56
Met Arg	
310	
 TCC ACC AGC ATC TTG ATC GGC CTT GTT GCC GGC GTC GCT GCT CAG AGC	104
Ser Thr Ser Ile Leu Ile Gly Leu Val Ala Gly Val Ala Ala Gln Ser	
315	320
	325
 TCT GGC TCT GGC CAT ACA ACC AGG TAC TGG GAC TGC TGC AAG CCC TCA	152
Ser Gly Ser Gly His Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser	
330	335
	340
 TGC GCC TGG GAT GAG AAG GCG GCT GTC AGC CGG CCG GTC ACA ACA TGC	200
Cys Ala Trp Asp Glu Lys Ala Ala Val Ser Arg Pro Val Thr Thr Cys	
345	350
	355
 GAC AGG AAC AAC AGC CCC CTT TCG CCC GGC GCT GTG AGC GGC TGC GAC	248
Asp Arg Asn Asn Ser Pro Leu Ser Pro Gly Ala Val Ser Gly Cys Asp	
360	365
	370
 CCC AAC GGC GTT GCA TTC ACC TGC AAC GAC AAC CAG CCT TGG GCC GTA	296
Pro Asn Gly Val Ala Phe Thr Cys Asn Asp Asn Gln Pro Trp Ala Val	
375	380
	385
	390
 AAC AAC AAT GTC GCC TAC GGT TTT GCG GCT ACC GCC TTC CCT GGT GGC	344
Asn Asn Asn Val Ala Tyr Gly Phe Ala Ala Thr Ala Phe Pro Gly Gly	
395	400
	405

AAT GAG GCG TCG TGG TGC TGT GCC TGC TAT GCT CTT CAA TTC ACA TCC Asn Glu Ala Ser Trp Cys Cys Ala Cys Tyr Ala Leu Gln Phe Thr Ser 410 415 420	392
GGC CCC GTT GCT GGC AAG ACG ATG GTT GTG CAA TCC ACC AAC ACT GGC Gly Pro Val Ala Gly Lys Thr Met Val Val Gln Ser Thr Asn Thr Gly 425 430 435	440
GGA GAT CTC AGC GGC ACT CAC TTC GAT ATC CAG ATG CCC GGT GGA GGT Gly Asp Leu Ser Gly Thr His Phe Asp Ile Gln Met Pro Gly Gly Gly 440 445 450	488
CTC GGC ATC TTC GAC GGC TGC ACC CCG CAG TTC GGC TTC ACG TTC CCC Leu Gly Ile Phe Asp Gly Cys Thr Pro Gln Phe Gly Phe Thr Phe Pro 455 460 465 470	536
GGC AAC CGC TAC GGC GGT ACC ACG AGC CGC AGC CAG TGC GCC GAG CTG Gly Asn Arg Tyr Gly Gly Thr Thr Ser Arg Ser Gln Cys Ala Glu Leu 475 480 485	584
CCC TCC GTC CTC CGT GAC GGC TGC CAC TGG CGT TAC GAC TGG TTC AAC Pro Ser Val Leu Arg Asp Gly Cys His Trp Arg Tyr Asp Trp Phe Asn 490 495 500	632
GAT GCC GAC AAC CCC AAC GTC AAC TGG CGC CGC GTC CGA TGC CCG GCG Asp Ala Asp Asn Pro Asn Val Asn Trp Arg Arg Val Arg Cys Pro Ala 505 510 515	680
GCC CTC ACG AAC CGC TCC GGC TGC GTC CGC AAC GAC GAC AAC AGC TAC Ala Leu Thr Asn Arg Ser Gly Cys Val Arg Asn Asp Asn Ser Tyr 520 525 530	728
CCC GTC TTC GAG CCC GGC ACG GGC ACC CCG CCG ACC CCC ACG ACC ACG Pro Val Phe Glu Pro Gly Thr Gly Thr Pro Pro Thr Pro Thr Thr Thr 535 540 545 550	776
ACT ACC AGC TCC CCT CCT CAG CCC ACC AAC GGC GGA GGC GGC GGC ACT Thr Thr Ser Ser Pro Pro Gln Pro Thr Asn Gly Gly Gly Gly Thr 555 560 565	824
TCT CCT CAC TGG GGC CAG TGC GGC GGC CAG GGC TGG TCT GGC CCG ACG Ser Pro His Trp Gly Gln Cys Gly Gly Gln Gly Trp Ser Gly Pro Thr 570 575 580	872
GCC TGT GCC GGT GGG TCG ACC TGC AAC CTG ATC AAC CCG TGG TAC TCC Ala Cys Ala Gly Gly Ser Thr Cys Asn Leu Ile Asn Pro Trp Tyr Ser 585 590 595	920
CAG TGC ATT CCC AAC TAAGTGATCC GGGCATTGCG GTCGAAAGGG GACCGTTAGT Gln Cys Ile Pro Asn 600	975
CGACAAGGCC CAGCCAGACC TCAGGCAGGT GGCTGCCATG GCAGATTGTA TATAGTCTTC	1035
CGAGTACATA CTATTGAATG AAAATAAGAG CGGCTGGAC CATGAGCAGA TGCCATTGAA	1095
TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1154

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Arg Ser Thr Ser Ile Leu Ile Gly Leu Val Ala Gly Val Ala Ala
1 5 10 15

Gln Ser Ser Gly Ser Gly His Thr Thr Arg Tyr Trp Asp Cys Cys Lys
20 25 30

Pro Ser Cys Ala Trp Asp Glu Lys Ala Ala Val Ser Arg Pro Val Thr
35 40 45

Thr Cys Asp Arg Asn Asn Ser Pro Leu Ser Pro Gly Ala Val Ser Gly
50 55 60

Cys Asp Pro Asn Gly Val Ala Phe Thr Cys Asn Asp Asn Gln Pro Trp
65 70 75 80

Ala Val Asn Asn Asn Val Ala Tyr Gly Phe Ala Ala Thr Ala Phe Pro
85 90 95

Gly Gly Asn Glu Ala Ser Trp Cys Cys Ala Cys Tyr Ala Leu Gln Phe
100 105 110

Thr Ser Gly Pro Val Ala Gly Lys Thr Met Val Val Gln Ser Thr Asn
115 120 125

Thr Gly Gly Asp Leu Ser Gly Thr His Phe Asp Ile Gln Met Pro Gly
130 135 140

Gly Gly Leu Gly Ile Phe Asp Gly Cys Thr Pro Gln Phe Gly Phe Thr
145 150 155 160

Phe Pro Gly Asn Arg Tyr Gly Gly Thr Thr Ser Arg Ser Gln Cys Ala
165 170 175

Glu Leu Pro Ser Val Leu Arg Asp Gly Cys His Trp Arg Tyr Asp Trp
180 185 190

Phe Asn Asp Ala Asp Asn Pro Asn Val Asn Trp Arg Arg Val Arg Cys
195 200 205

Pro Ala Ala Leu Thr Asn Arg Ser Gly Cys Val Arg Asn Asp Asp Asn
210 215 220

Ser Tyr Pro Val Phe Glu Pro Gly Thr Gly Thr Pro Pro Thr Pro Thr
225 230 235 240

Thr Thr Thr Ser Ser Pro Pro Gln Pro Thr Asn Gly Gly Gly Gly
245 250 255

Gly Thr Ser Pro His Trp Gly Gln Cys Gly Gly Gln Gly Trp Ser Gly
260 265 270

Pro Thr Ala Cys Ala Gly Gly Ser Thr Cys Asn Leu Ile Asn Pro Trp
275 280 285

Tyr Ser Gln Cys Ile Pro Asn
290 295

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 110..1156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAAGTTCTGG CCGAACAGA TCTCCGTTGT CGATCTTCGA TTTTCCAGAC TCAGTCTGTG 60

ACACTCCTTC AATCCACATT CCTTTACTTC TTTCGTCACTC ATTCACATC ATG ATT 115
Met Ile

TCA GCT TGG ATT CTC CTG GGG CTG GTA GGC GCC GTG CCC TCC TCC GTC 163
Ser Ala Trp Ile Leu Leu Gly Leu Val Gly Ala Val Pro Ser Ser Val
300 305 310

ATG GCC GCC TCG GGC AAA GGC CAC ACC ACC CGC TAC TGG GAT TGC TGC 211
Met Ala Ala Ser Gly Lys Gly His Thr Thr Arg Tyr Trp Asp Cys Cys
315 320 325

AAG ACT TCT TGC GCA TGG GAG GGC AAG GCA TCC GTC TCC GAG CCT GTC 259
Lys Thr Ser Cys Ala Trp Glu Gly Lys Ala Ser Val Ser Glu Pro Val
330 335 340 345

CTG ACC TGT AAC AAG CAG GAC AAC CCC ATC GTC GAT GCC AAC GCC AGA 307
Leu Thr Cys Asn Lys Gln Asp Asn Pro Ile Val Asp Ala Asn Ala Arg
350 355 360

AGC GGC TGC GAC GGC GGC GGG GCA TTT GCC TGT ACC AAC AAT TCC CCT 355
Ser Gly Cys Asp Gly Gly Ala Phe Ala Cys Thr Asn Asn Ser Pro
365 370 375

TGG	GCC	GTG	AGC	GAG	GAC	CTG	GCC	TAC	GGA	TTT	GCT	GCC	ACA	GCC	CTC		403
Trp	Ala	Val	Ser	Glu	Asp	Leu	Ala	Tyr	Gly	Phe	Ala	Ala	Thr	Ala	Leu		
380				385						390							
AGC	GGC	GGC	ACT	GAG	GGC	AGC	TGG	TGC	TGC	GCG	TGT	TAC	GCC	ATC	ACA		451
Ser	Gly	Gly	Thr	Glu	Gly	Ser	Trp	Cys	Cys	Ala	Cys	Tyr	Ala	Ile	Thr		
395				400						405							
TTC	ACG	AGT	GGC	CCT	GTG	GCT	GGC	AAG	AAG	ATG	GTC	GTC	CAG	TCC	ACG		499
Phe	Thr	Ser	Gly	Pro	Val	Ala	Gly	Lys	Lys	Met	Val	Val	Gln	Ser	Thr		
410				415				420			425						
AAC	ACG	GGA	GGC	GAC	CTG	TCC	AAC	AAC	CAC	TTT	GAC	CTG	ATG	ATT	CCC		547
Asn	Thr	Gly	Gly	Asp	Leu	Ser	Asn	Asn	His	Phe	Asp	Leu	Met	Ile	Pro		
				430				435			440						
GGT	GGA	GGC	CTC	GGC	ATC	TTT	GAC	GGT	TGC	TCG	GCT	CAG	TTC	GGA	CAA		595
Gly	Gly	Gly	Leu	Gly	Ile	Phe	Asp	Gly	Cys	Ser	Ala	Gln	Phe	Gly	Gln		
				445				450			455						
CTT	CTT	CCC	GGC	GAG	CGT	TAC	GGA	GGT	GTT	TCG	TCC	CGC	TCT	CAA	TGC		643
Leu	Leu	Pro	Gly	Glu	Arg	Tyr	Gly	Gly	Val	Ser	Ser	Arg	Ser	Gln	Cys		
				460				465			470						
GAT	GGC	ATG	CCC	GAG	CTC	TTG	AAA	GAC	GGT	TGC	CAG	TGG	CGC	TTC	GAC		691
Asp	Gly	Met	Pro	Glu	Leu	Leu	Lys	Asp	Gly	Cys	Gln	Trp	Arg	Phe	Asp		
				475				480			485						
TGG	TTC	AAG	AAC	TCA	GAC	AAC	CCT	GAC	ATC	GAG	TTC	GAG	CAG	GTC	CAG		739
Trp	Phe	Lys	Asn	Ser	Asp	Asn	Pro	Asp	Ile	Glu	Phe	Glu	Gln	Val	Gln		
				490				495			500			505			
TGT	CCC	AAA	GAG	CTC	ATT	GCG	GTC	TCT	GGG	TGC	GTC	CGT	GAC	GAC	GAT		787
Cys	Pro	Lys	Glu	Leu	Ile	Ala	Val	Ser	Gly	Cys	Val	Arg	Asp	Asp	Asp		
				510				515			520						
AGC	AGC	TTT	CCC	GTC	TTC	CAA	GGT	TCG	GGC	TCA	GGA	GAT	GTC	AAC	CCA		835
Ser	Ser	Phe	Pro	Val	Phe	Gln	Gly	Ser	Gly	Ser	Gly	Asp	Val	Asn	Pro		
				525				530			535						
CCT	CCC	AAG	CCG	ACT	ACG	ACT	ACG	ACC	TCG	TCA	AAG	CCG	AAA	ACA	ACC		883
Pro	Pro	Lys	Pro	Thr	Thr	Thr	Thr	Thr	Ser	Ser	Lys	Pro	Lys	Thr	Thr		
				540				545			550						
TCT	GCA	CCA	TCC	ACT	CTC	TCG	AAC	CCA	TCC	GCC	CCT	CAA	CAG	CCA	GGG		931
Ser	Ala	Pro	Ser	Thr	Leu	Ser	Asn	Pro	Ser	Ala	Pro	Gln	Gln	Pro	Gly		
				555				560			565						
AAC	ACT	GAT	AGA	CCT	GCC	GAG	ACA	ACC	ACT	ACC	AAG	CTG	CCT	GCC	CTG		979
Asn	Thr	Asp	Arg	Pro	Ala	Glu	Thr	Thr	Thr	Thr	Lys	Leu	Pro	Ala	Leu		
				570				575			580			585			
CCG	GCC	ACG	ACG	AGC	AGC	CCT	GCT	GTC	TCA	GTT	CCT	TCG	TCC	AGC	GCT		1027
Pro	Ala	Thr	Thr	Ser	Ser	Pro	Ala	Val	Ser	Val	Pro	Ser	Ser	Ser	Ala		
				590				595			600						

CGC GTG CCT TTG TGG GGG CAA TGC GAC TCG GAA GCT TCA TGG GAC GCA Arg Val Pro Leu Trp Gly Gln Cys Asp Ser Glu Ala Ser Trp Asp Ala	605 610 615	1075
CCT AAG AAG TGT GCA AAG GGC ACC AAG TGT GTC TAC GTC AAC GAC TGG Pro Lys Lys Cys Ala Lys Gly Thr Lys Cys Val Tyr Val Asn Asp Trp	620 625 630	1123
TAC TCT CAA TGC CAG CCG AAG AAC TCT TGT GCT TGAGAAGCAA TGCTCACAGC Tyr Ser Gln Cys Gln Pro Lys Asn Ser Cys Ala	635 640	1176
ATGTCCTCTT GTCACCCCTT CTTTCATTC CCAAACATAC TTACTGTATT ATTATTTCG		1236
ATGCTTCATT TCTTGCTTGT TTCTGTCTTT CCTGCACGCA GCTTTCAACG ATACCCTTCA		1296
TGCGATTGCC CTACGATCAG ATGATGGGCA CGACATGGAG GATGGTTGG GCACTCACGC		1356
GTTCAGGACG GGAAAATTAA TTAGGGCTGA GATCCGTGAA TTGACTTCAT TTCGGCGGAA		1416
TGTCTGC		1423

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ile Ser Ala Trp Ile Leu Leu Gly Leu Val Gly Ala Val Pro Ser		
1 5 10 15		
Ser Val Met Ala Ala Ser Gly Lys Gly His Thr Thr Arg Tyr Trp Asp		
20 25 30		
Cys Cys Lys Thr Ser Cys Ala Trp Glu Gly Lys Ala Ser Val Ser Glu		
35 40 45		
Pro Val Leu Thr Cys Asn Lys Gln Asp Asn Pro Ile Val Asp Ala Asn		
50 55 60		
Ala Arg Ser Gly Cys Asp Gly Gly Ala Phe Ala Cys Thr Asn Asn		
65 70 75 80		
Ser Pro Trp Ala Val Ser Glu Asp Leu Ala Tyr Gly Phe Ala Ala Thr		
85 90 95		
Ala Leu Ser Gly Gly Thr Glu Gly Ser Trp Cys Cys Ala Cys Tyr Ala		
100 105 110		
Ile Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Val Val Gln		
115 120 125		

Ser Thr Asn Thr Gly Gly Asp Leu Ser Asn Asn His Phe Asp Leu Met
 130 135 140

Ile Pro Gly Gly Gly Leu Gly Ile Phe Asp Gly Cys Ser Ala Gln Phe
 145 150 155 160

Gly Gln Leu Leu Pro Gly Glu Arg Tyr Gly Gly Val Ser Ser Arg Ser
 165 170 175

Gln Cys Asp Gly Met Pro Glu Leu Leu Lys Asp Gly Cys Gln Trp Arg
 180 185 190

Phe Asp Trp Phe Lys Asn Ser Asp Asn Pro Asp Ile Glu Phe Glu Gln
 195 200 205

Val Gln Cys Pro Lys Glu Leu Ile Ala Val Ser Gly Cys Val Arg Asp
 210 215 220

Asp Asp Ser Ser Phe Pro Val Phe Gln Gly Ser Gly Ser Gly Asp Val
 225 230 235 240

Asn Pro Pro Pro Lys Pro Thr Thr Thr Ser Ser Lys Pro Lys
 245 250 255

Thr Thr Ser Ala Pro Ser Thr Leu Ser Asn Pro Ser Ala Pro Gln Gln
 260 265 270

Pro Gly Asn Thr Asp Arg Pro Ala Glu Thr Thr Thr Lys Leu Pro
 275 280 285

Ala Leu Pro Ala Thr Thr Ser Ser Pro Ala Val Ser Val Pro Ser Ser
 290 295 300

Ser Ala Arg Val Pro Leu Trp Gly Gln Cys Asp Ser Glu Ala Ser Trp
 305 310 315 320

Asp Ala Pro Lys Lys Cys Ala Lys Gly Thr Lys Cys Val Tyr Val Asn
 325 330 335

Asp Trp Tyr Ser Gln Cys Gln Pro Lys Asn Ser Cys Ala
 340 345

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 60..956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGCAGCACC CCTCAAGCTG TACAGTTCC ACCCCGCTCT CTTTCTTCG GCCCCCAGG	59
ATG CGC TCT ACT CCC GTT CTT CGC ACA ACC CTG GCC GCT GCA CTT CCT Met Arg Ser Thr Pro Val Leu Arg Thr Thr Leu Ala Ala Ala Leu Pro	107
350.....355.....360.....365	
CTG GTC GCC TCC GCG GCC AGT GGC AGT GGC CAG TCC ACG AGA TAC TGG Leu Val Ala Ser Ala Ala Ser Gly Ser Gly Gln Ser Thr Arg Tyr Trp	155
370.....375.....380	
GAC TGC TGC AAG CCG TCG TGC GCT TGG CCC GGG AAG GCC GCC GTC AGC Asp Cys Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Ala Ala Val Ser	203
385.....390.....395	
CAA CCG GTC TAC GCG TGC GAT GCC AAC TTC CAG CGC CTG TCC GAC TTC Gln Pro Val Tyr Ala Cys Asp Ala Asn Phe Gln Arg Leu Ser Asp Phe	251
400.....405.....410	
AAT GTC CAG TCG GGC TGC AAC GGC GGC TCG GCC TAC TCC TGC GCC GAC Asn Val Gln Ser Gly Cys Asn Gly Ser Ala Tyr Ser Cys Ala Asp	299
415.....420.....425	
CAG ACT CCC TGG GCG GTG AAC GAC AAT CTC GCC TAC GGC TTC GCC GCG Gln Thr Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala	347
430.....435.....440.....445	
ACG AGC ATC GCC GGC GGG TCC GAA TCC TCG TGG TGC TGC GCC TGC TAC Thr Ser Ile Ala Gly Gly Ser Glu Ser Ser Trp Cys Cys Ala Cys Tyr	395
450.....455.....460	
GCG CTC ACC TTC ACT TCC GGT CCC GTC GCC GGC AAG ACA ATG GTG GTG Ala Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Thr Met Val Val	443
465.....470.....475	
CAG TCA ACG AGC ACT GGC GGC GAC CTG GGA AGT AAC CAG TTC GAT ATC Gln Ser Thr Ser Thr Gly Gly Asp Leu Gly Ser Asn Gln Phe Asp Ile	491
480.....485.....490	
GCC ATG CCC GGC GGC GTG GGC ATC TTC AAC GGC TGC AGC TCG CAG Ala Met Pro Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Ser Gln	539
495.....500.....505	
TTC GGC GGC CTC CCC GGC GCT CAA TAC GGC GGC ATT TCG TCG CGC GAC Phe Gly Gly Leu Pro Gly Ala Gln Tyr Gly Ile Ser Ser Arg Asp	587
510.....515.....520.....525	
CAG TGC GAT TCC TTC CCC GCG CCG CTC AAG CCC GGC TGC CAG TGG CGG Gln Cys Asp Ser Phe Pro Ala Pro Leu Lys Pro Gly Cys Gln Trp Arg	635
530.....535.....540	
TTT GAC TGG TTC CAG AAC GCC GAC AAC CCG ACG TTC ACG TPC CAG CAG Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Thr Phe Thr Phe Gln Gln	683
545.....550.....555	

GTG CAG TGC CCC GCC GAG ATC GTT GCC CGC TCC GGC TGC AAG CGC AAC	731
Val Gln Cys Pro Ala Glu Ile Val Ala Arg Ser Gly Cys Lys Arg Asn	
560 565 570	
GAC GAC TCC AGC TTC CCC GTC TTC ACC CCC CCA AGC GGT GGC AAC GGT	779
Asp Asp Ser Ser Phe Pro Val Phe Thr Pro Pro Ser Gly Gly Asn Gly	
575 580 585	
GGC ACC GGG ACG CCC ACG TCG ACT GCG CCT GGG TCG GGC CAG ACG TCT	827
Gly Thr Gly Thr Pro Thr Ser Thr Ala Pro Gly Ser Gly Gln Thr Ser	
590 595 600 605	
CCC GGC GGC GGC AGT GGC TGC ACG TCT CAG AAG TGG GCT CAG TGC GGT	875
Pro Gly Gly Ser Gly Cys Thr Ser Gln Lys Trp Ala Gln Cys Gly	
610 615 620	
GGC ATC GGC TTC AGC GGA TGC ACC ACC TGT GTC TCT GGC ACC ACC TGC	923
Gly Ile Gly Phe Ser Gly Cys Thr Thr Cys Val Ser Gly Thr Thr Cys	
625 630 635	
CAG AAG TTG AAC GAC TAC TAC TCG CAG TGC CTC TAAACAGCTT TTTCGCACGAG	976'
Gln Lys Leu Asn Asp Tyr Tyr Ser Gln Cys Leu	
640 645	
GTGGCGGGAC GGAGCAAGGA GACCGTCAAC TTTCGTATGC ATATTTTTG AGCGCTCAAT	1036
ACATACATAA CCTTCGATTC TTGTACATAG CACGCCGTA CACATCTCAC ACCGACTTTG	1096
GGGGCGGAAT CAGGCCGTT TTAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	1156
AAAAAAAAA AAAAAAA	1174

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Arg Ser Thr Pro Val Leu Arg Thr Thr Leu Ala Ala Ala Leu Pro	
1 5 10 15	
Leu Val Ala Ser Ala Ala Ser Gly Ser Gly Gln Ser Thr Arg Tyr Trp	
20 25 30	
Asp Cys Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Ala Ala Val Ser	
35 40 45	
Gln Pro Val Tyr Ala Cys Asp Ala Asn Phe Gln Arg Leu Ser Asp Phe	
50 55 60	

Asn	Val	Gln	Ser	Gly	Cys	Asn	Gly	Gly	Ser	Ala	Tyr	Ser	Cys	Ala	Asp
65						70				75				80	
<hr/>															
Gln	Thr	Pro	Trp	Ala	Val	Asn	Asp	Asn	Leu	Ala	Tyr	Gly	Phe	Ala	Ala
						85			90					95	
<hr/>															
Thr	Ser	Ile	Ala	Gly	Gly	Ser	Glu	Ser	Ser	Trp	Cys	Cys	Ala	Cys	Tyr
						100		105						110	
<hr/>															
Ala	Leu	Thr	Phe	Thr	Ser	Gly	Pro	Val	Ala	Gly	Lys	Thr	Met	Val	Val
							115		120			125			
<hr/>															
Gln	Ser	Thr	Ser	Thr	Gly	Gly	Asp	Leu	Gly	Ser	Asn	Gln	Phe	Asp	Ile
							130		135			140			
<hr/>															
Ala	Met	Pro	Gly	Gly	Gly	Val	Gly	Ile	Phe	Asn	Gly	Cys	Ser	Ser	Gln
						145		150			155			160	
<hr/>															
Phe	Gly	Gly	Leu	Pro	Gly	Ala	Gln	Tyr	Gly	Gly	Ile	Ser	Ser	Arg	Asp
						165			170			175			
<hr/>															
Gln	Cys	Asp	Ser	Phe	Pro	Ala	Pro	Leu	Lys	Pro	Gly	Cys	Gln	Trp	Arg
						180			185			190			
<hr/>															
Phe	Asp	Trp	Phe	Gln	Asn	Ala	Asp	Asn	Pro	Thr	Phe	Thr	Phe	Gln	Gln
						195			200			205			
<hr/>															
Val	Gln	Cys	Pro	Ala	Glu	Ile	Val	Ala	Arg	Ser	Gly	Cys	Lys	Arg	Asn
						210		215			220				
<hr/>															
Asp	Asp	Ser	Ser	Phe	Pro	Val	Phe	Thr	Pro	Pro	Ser	Gly	Gly	Asn	Gly
						225		230			235			240	
<hr/>															
Gly	Thr	Gly	Thr	Pro	Thr	Ser	Thr	Ala	Pro	Gly	Ser	Gly	Gln	Thr	Ser
						245			250			255			
<hr/>															
Pro	Gly	Gly	Ser	Gly	Cys	Thr	Ser	Gln	Lys	Trp	Ala	Gln	Cys	Gly	
						260			265			270			
<hr/>															
Gly	Ile	Gly	Phe	Ser	Gly	Cys	Thr	Thr	Cys	Val	Ser	Gly	Thr	Thr	Cys
						275			280			285			
<hr/>															
Gln	Lys	Leu	Asn	Asp	Tyr	Tyr	Ser	Gln	Cys	Leu					
						290			295						

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 913 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 41..706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCAC TATTCT CAGCTCCATT CTCCCTTGAA GTAATTCA CC	ATG TTC TCT CCG CTC	55
Met Phe Ser Pro Leu		
300		
TGG GCC CTG TCG GCT CTG CTC CTA TTT CCT GCC ACT GAA GCC ACT AGC		103
Trp Ala Leu Ser Ala Leu Leu Phe Pro Ala Thr Glu Ala Thr Ser		
305 310 315 320		
GGC GTG ACA ACC AGG TAC TGG GAC TGC TGC AAG CCG TCT TGT GCT TGG		151
Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp		
325 330 335		
ACG GGC AAA GCA TCC GTC TCC AAG CCC GTC GGA ACC TGC GAC ATC AAC		199
Thr Gly Lys Ala Ser Val Ser Lys Pro Val Gly Thr Cys Asp Ile Asn		
340 345 350		
GAC AAC GCC CAG CCG AGC GAT CTG CTC AAG TCG TCC TGT GAT GGC		247
Asp Asn Ala Gln Thr Pro Ser Asp Leu Leu Lys Ser Ser Cys Asp Gly		
355 360 365		
GGC AGC GCC TAC TAC TGC AGC AAC CAG GGC CCA TGG GCC GTG AAC GAC		295
Gly Ser Ala Tyr Tyr Cys Ser Asn Gln Gly Pro Trp Ala Val Asn Asp		
370 375 380		
AGC CTT TCC TAC GGC TTC GCT GCC GCC AAG CTG TCC GGA AAG CAG GAG		343
Ser Leu Ser Tyr Gly Phe Ala Ala Lys Leu Ser Gly Lys Gln Glu		
385 390 395 400		
ACT GAT TGG TGC TGT GGC TGC TAC AAG CTC ACA TTC ACC TCC ACC GCC		391
Thr Asp Trp Cys Cys Gly Cys Tyr Lys Leu Thr Phe Thr Ser Thr Ala		
405 410 415		
GTT TCC GGC AAG CAA ATG ATC GTG CAA ATC ACG AAC ACG GGC GGC GAC		439
Val Ser Gly Lys Gln Met Ile Val Gln Ile Thr Asn Thr Gly Gly Asp		
420 425 430		
CTC GGC AAC AAC CAC TTC GAC ATC GCC ATG CCG GGC GGC GGC GTC GGC		487
Leu Gly Asn Asn His Phe Asp Ile Ala Met Pro Gly Gly Val Gly		
435 440 445		
ATC TTC AAC GGG TGC TCC AAG CAA TGG AAC GGC ATC AAT CTG GGC AAC		535
Ile Phe Asn Gly Cys Ser Lys Gln Trp Asn Gly Ile Asn Leu Gly Asn		
450 455 460		
CAG TAT GGC GGC TTC ACT GAC CGC TCG CAA TGT GCG ACG CTC CCG TCC		583
Gln Tyr Gly Gly Phe Thr Asp Arg Ser Gln Cys Ala Thr Leu Pro Ser		
465 470 475 480		
AAG TGG CAG GCC AGC TGC AAC TGG CGC TTC GAC TGG TTC GAG AAT GCC		631
Lys Trp Gln Ala Ser Cys Asn Trp Arg Phe Asp Trp Phe Glu Asn Ala		
485 490 495		

GAC AAC CCC ACC GTC GAT TGG GAG CCT GTC ACT TGC CCA CAG GAA TTG	679	
Asp Asn Pro Thr Val Asp Trp Glu Pro Val Thr Cys Pro Gln Glu Leu		
500	505	510
 GTC GCC CGG ACT GGC TGT TCC CGT ACC TAAGTGGGGG TGGAACCTCC	726	
Val Ala Arg Thr Gly Cys Ser Arg Thr		
515	520	
 ATGTGAATTG GTGTATATAG CTCTGCCTG AGCATCCACC AGTCGCATG TGTTGATCAG	786	
GAGTTGTGTT GCCTTGCTAG GAAAGACTTT GTTGGAAACT TGCCTGTTA TTCCAATTGA	846	
 ATAACCCTGT ATAGACCGGT CACATTTTC TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA	906	
AAAAAAA	913	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Phe Ser Pro Leu Trp Ala Leu Ser Ala Leu Leu Leu Phe Pro Ala				
1	5	10	15	
 Thr Glu Ala Thr Ser Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys				
	20	25	30	
 Pro Ser Cys Ala Trp Thr Gly Lys Ala Ser Val Ser Lys Pro Val Gly				
	35	40	45	
 Thr Cys Asp Ile Asn Asp Asn Ala Gln Thr Pro Ser Asp Leu Leu Lys				
	50	55	60	
 Ser Ser Cys Asp Gly Gly Ser Ala Tyr Tyr Cys Ser Asn Gln Gly Pro				
	65	70	75	80
 Trp Ala Val Asn Asp Ser Leu Ser Tyr Gly Phe Ala Ala Ala Lys Leu				
	85	90	95	
 Ser Gly Lys Gln Glu Thr Asp Trp Cys Cys Gly Cys Tyr Lys Leu Thr				
	100	105	110	
 Phe Thr Ser Thr Ala Val Ser Gly Lys Gln Met Ile Val Gln Ile Thr				
	115	120	125	
 Asn Thr Gly Gly Asp Leu Gly Asn Asn His Phe Asp Ile Ala Met Pro				
	130	135	140	
 Gly Gly Gly Val Gly Ile Phe Asn Gly Cys Ser Lys Gln Trp Asn Gly				
	145	150	155	160

Ile Asn Leu Gly Asn Gln Tyr Gly Gly Phe Thr Asp Arg Ser Gln Cys
165 170 175

Ala Thr Leu Pro Ser Lys Trp Gln Ala Ser Cys Asn Trp Arg Phe Asp
180 185 190

Trp Phe Glu Asn Ala Asp Asn Pro Thr Val Asp Trp Glu Pro Val Thr
195 200 205

Cys Pro Gln Glu Leu Val Ala Arg Thr Gly Cys Ser Arg Thr
210 215 220

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 808 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 37..714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGCTGCTGG GTATATAATG CTCAGACTTG GAACCA ATG GTC CAT CCA AAC ATG 54
Met Val His Pro Asn Met
225

CTT AAA ACG CTC GCT CCA TTG ATC ATC TTG GCC GCC TCG GTC ACA GCG 102
Leu Lys Thr Leu Ala Pro Leu Ile Ile Leu Ala Ala Ser Val Thr Ala
230 235 240

CAA ACA GCA GGA GTT ACG ACC CGC TAC TGG GAC TGC TGC AAG CCA AGC 150
Gln Thr Ala Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser
245 250 255 260

TGT GGA TGG AGT GGA AAG GCT TCT GTT TCT GCT CCA GTC AGA ACT TGC 198
Cys Gly Trp Ser Gly Lys Ala Ser Val Ser Ala Pro Val Arg Thr Cys
265 270 275

GAT CGT AAT GGA AAT ACA CTT GGC CCA GAC GTG AAA AGC GGA TGT GAT 246
Asp Arg Asn Gly Asn Thr Leu Gly Pro Asp Val Lys Ser Gly Cys Asp
280 285 290

AGC GGT GGA ACG TCA TTC ACT TGC GCG AAC AAT GGT CCA TTT GCG ATT 294
Ser Gly Gly Thr Ser Phe Thr Cys Ala Asn Asn Gly Pro Phe Ala Ile
295 300 305

GAC AAT AAC ACT GCA TAT GGT TTT GCT GCA GCC CAC TTA GCG GGC TCT 342
Asp Asn Asn Thr Ala Tyr Gly Phe Ala Ala Ala His Leu Ala Gly Ser
310 315 320

AGC GAA GCA GCC TGG TGT TGC CAG TGC TAC GAA TTG ACG TTT ACG AGT 390
 Ser Glu Ala Ala Trp Cys Cys Gln Cys Tyr Glu Leu Thr Phe Thr Ser
 325 330 335 340
 GGA CCC GTA GTT GGG AAG AAA CTG ACC GTT CAA GTC ACA AAC ACG GGA 438
 Gly Pro Val Val Gly Lys Lys Leu Thr Val Gln Val Thr Asn Thr Gly
 345 350 355
 GGT GAC CTC GGA AAT AAT CAC TTT GAC CTG ATG ATC CCC GGT GGA GGT 486
 Gly Asp Leu Gly Asn Asn His Phe Asp Leu Met Ile Pro Gly Gly
 360 365 370
 GTT GGC CTC TTC ACA CAA GGA TGT CCT GCT CAG TTT GGG AGC TGG AAC 534
 Val Gly Leu Phe Thr Gln Gly Cys Pro Ala Gln Phe Gly Ser Trp Asn
 375 380 385
 GGG GGT GCT CAA TAC GGG GGT GTG TCC AGC CGT GAC CAA TGC TCC CAA 582
 Gly Gly Ala Gln Tyr Gly Gly Val Ser Ser Arg Asp Gln Cys Ser Gln
 390 395 400
 CTT CCA GCA GCT GTG CAA GCT GGA TGT CAA TTC CGT TTC GAC TGG ATG 630
 Leu Pro Ala Ala Val Gln Ala Gly Cys Gln Phe Arg Phe Asp Trp Met
 405 410 415 420
 GGT GGC GCG GAT AAC CCC AAC GTC ACC TTC CGA CCT GTG ACC TGC CCA 678
 Gly Gly Ala Asp Asn Pro Asn Val Thr Phe Arg Pro Val Thr Cys Pro
 425 430 435
 GCG CAG CTC ACT AAT ATC TCG GGC TGT GTT CGT AAA TGATTCACGA 724
 Ala Gln Leu Thr Asn Ile Ser Gly Cys Val Arg Lys
 440 445
 ATATGTAGTG TCGAATATGT ACATGTGTAT GTACTATAGC TTCAAAGATG GAGGGTCTGT 784
 TTA..... AAA..... AAAA 808

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Val His Pro Asn Met Leu Lys Thr Leu Ala Pro Leu Ile Ile Leu
 1 5 10 15

Ala Ala Ser Val Thr Ala Gln Thr Ala Gly Val Thr Thr Arg Tyr Trp
 20 25 30

Asp Cys Cys Lys Pro Ser Cys Gly Trp Ser Gly Lys Ala Ser Val Ser
 35 40 45

Ala Pro Val Arg Thr Cys Asp Arg Asn Gly Asn Thr Leu Gly Pro Asp
 50 55 60

Val Lys Ser Gly Cys Asp Ser Gly Gly Thr Ser Phe Thr Cys Ala Asn
 65 70 75 80

Asn Gly Pro Phe Ala Ile Asp Asn Asn Thr Ala Tyr Gly Phe Ala Ala
 85 90 95

Ala His Leu Ala Gly Ser Ser Glu Ala Ala Trp Cys Cys Gln Cys Tyr
 100 105 110

Glu Leu Thr Phe Thr Ser Gly Pro Val Val Gly Lys Lys Leu Thr Val
 115 120 125

Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Asn Asn His Phe Asp Leu
 130 135 140

Met Ile Pro Gly Gly Val Gly Leu Phe Thr Gln Gly Cys Pro Ala
 145 150 155 160

Gln Phe Gly Ser Trp Asn Gly Gly Ala Gln Tyr Gly Val Ser Ser
 165 170 175

Arg Asp Gln Cys Ser Gln Leu Pro Ala Ala Val Gln Ala Gly Cys Gln
 180 185 190

Phe Arg Phe Asp Trp Met Gly Gly Ala Asp Asn Pro Asn Val Thr Phe
 195 200 205

Arg Pro Val Thr Cys Pro Ala Gln Leu Thr Asn Ile Ser Gly Cys Val
 210 215 220

Arg Lys
 225

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1048 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 13..906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTTGGAAC CA ATG GTC CAT CCA AAC ATG CTT AAA ACG CTC GCT CCA
 Met Val His Pro Asn Met Leu Lys Thr Leu Ala Pro
 230 235

48

TTG ATC ATC TTG GCC GCC TCG GTC ACA GCG CAA ACA GCA GGA GTT ACG	96
Leu Ile Ile Leu Ala Ala Ser Val Thr Ala Gln Thr Ala Gly Val Thr	
240 245 250	
ACC CGC TAC TGG GAC TGC TGC AAG CCA AGC TGT GGA TGG AGT GGA AAG	144
Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Gly Trp Ser Gly Lys	
255 260 265 270	
GCT TCT GTT TCT GCT CCA GTC AGA ACT TGC GAT CGT AAT GGA AAT ACA	192
Ala Ser Val Ser Ala Pro Val Arg Thr Cys Asp Arg Asn Gly Asn Thr	
275 280 285	
CTT GGC CCA GAC GTG AAA AGC GGA TGT GAT AGC GGT GGA ACG TCA TTC	240
Leu Gly Pro Asp Val Lys Ser Gly Cys Asp Ser Gly Gly Thr Ser Phe	
290 295 300	
ACT TGC GCG AAC AAT GGT CCA TTT GCG ATT GAC AAT AAC ACT GCA TAT	288
Thr Cys Ala Asn Asn Gly Pro Phe Ala Ile Asp Asn Asn Thr Ala Tyr	
305 310 315	
GGT TTT GCT GCA GCC CAC TTA GCG GGC TCT AGC GAA GCA GCC TGG TGT	336
Gly Phe Ala Ala Ala His Leu Ala Gly Ser Ser Glu Ala Ala Trp Cys	
320 325 330	
TGC CAG TGC TAC GAA TTG ACG TTT ACG AGT GGA CCC GTA GTT GGG AAG	384
Cys Gln Cys Tyr Glu Leu Thr Phe Thr Ser Gly Pro Val Val Gly Lys	
335 340 345 350	
AAA CTG ACC GTT CAA GTC ACA AAC ACG GGA GGT GAC CTC GGA AAT AAT	432
Lys Leu Thr Val Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Asn Asn	
355 360 365	
CAC TTT GAC CTG ATG ATC CCC GGT GGA GGT GTT GGC CTC TTC ACA CAA	480
His Phe Asp Leu Met Ile Pro Gly Gly Val Gly Leu Phe Thr Gln	
370 375 380	
GGA TGT CCT GCT CAG TTT GGG AGC TGG AAC GGG GGT GCT CAA TAC GGG	528
Gly Cys Pro Ala Gln Phe Gly Ser Trp Asn Gly Gly Ala Gln Tyr Gly	
385 390 395	
GGT GTG TCC AGC CGT GAC CAA TGC TCC CAA CTT CCA GCA GCT GTG CAA	576
Gly Val Ser Ser Arg Asp Gln Cys Ser Gln Leu Pro Ala Ala Val Gln	
400 405 410	
GCT GGA TGT CAA TTC CGT TTC GAC TGG ATG GGT GGC GCG GAT AAC CCC	624
Ala Gly Cys Gln Phe Arg Phe Asp Trp Met Gly Gly Ala Asp Asn Pro	
415 420 425 430	
AAC GTC ACC TTC CGA CCT GTG ACC TGC CCA GCG CAG CTC ACT AAT ATC	672
Asn Val Thr Phe Arg Pro Val Thr Cys Pro Ala Gln Leu Thr Asn Ile	
435 440 445	
TCG GGC TGT GTT CGT AAA CCC TCC AGC AGC ACC AGC TCT CCG GTC AAC	720
Ser Gly Cys Val Arg Lys Pro Ser Ser Ser Thr Ser Ser Pro Val Asn	
450 455 460	

CAG CCT ACC AGC ACC AGC ACC ACG TCC ACC TCC ACC ACC TCG AGC CCG	768
Gln Pro Thr Ser Thr Ser Thr Ser Thr Ser Thr Ser Ser Pro	
465 470 475	
CCA GTC CAG CCT ACG ACT CCC AGC GGC TGC ACT GCT GAG AGG TGG GCT	816
Pro Val Gln Pro Thr Thr Pro Ser Gly Cys Thr Ala Glu Arg Trp Ala	
480 485 490	
CAG TGC GGC GGC AAT GGC TGG AGC GGC TGC ACC ACC TGC GTC GCT GGC	864
Gln Cys Gly Gly Asn Gly Trp Ser Gly Cys Thr Thr Cys Val Ala Gly	
495 500 505 510	
AGC ACT TGC ACG AAG ATT AAT GAC TGG TAC CAT CAG TGC CTG	906
Ser Thr Cys Thr Lys Ile Asn Asp Trp Tyr His Gln Cys Leu	
515 520	
TAGACGCAGG GCAGCTTGAG GGCCTTACTG GTGGCGCAAC GAAATGACAC TCCCAATCAC	966
TGTATTAGTT CTTGTACATA ATTTCGTCAT CCCTCCAGGG ATTGTCACAT AAATGCAATG	1026
AGGAACAATG AGTACAGAAT TC	1048

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: protein
 - xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Val His Pro Asn Met	Leu Lys Thr	Leu Ala Pro	Leu Ile Ile Leu
1	5	10	15
Ala Ala Ser Val Thr Ala Gln	Thr Ala Gly Val	Thr Thr Arg Tyr Trp	
20	25	30	
Asp Cys Cys Lys Pro Ser Cys	Gly Trp Ser Gly Lys	Ala Ser Val Ser	
35	40	45	
Ala Pro Val Arg Thr Cys Asp	Arg Asn Gly Asn	Thr Leu Gly Pro Asp	
50	55	60	
Val Lys Ser Gly Cys Asp Ser	Gly Gly Thr Ser Phe	Thr Cys Ala Asn	
65	70	75	80
Asn Gly Pro Phe Ala Ile Asp	Asn Asn Thr Ala Tyr	Gly Phe Ala Ala	
85	90	95	
Ala His Leu Ala Gly Ser Ser	Glu Ala Ala Trp	Cys Cys Gln Cys Tyr	
100	105	110	
Glu Leu Thr Phe Thr Ser Gly	Pro Val Val Gly	Lys Lys Leu Thr Val	
115	120	125	

Gln Val Thr Asn Thr Gly Gly Asp Leu Gly Asn Asn His Phe Asp Leu
 130 135 140

Met Ile Pro Gly Gly Val Gly Leu Phe Thr Gln Gly Cys Pro Ala
 145 150 155 160

Gln Phe Gly Ser Trp Asn Gly Gly Ala Gln Tyr Gly Gly Val Ser Ser
 165 170 175

Arg Asp Gln Cys Ser Gln Leu Pro Ala Ala Val Gln Ala Gly Cys Gln
 180 185 190

Phe Arg Phe Asp Trp Met Gly Ala Asp Asn Pro Asn Val Thr Phe
 195 200 205

Arg Pro Val Thr Cys Pro Ala Gln Leu Thr Asn Ile Ser Gly Cys Val
 210 215 220

Arg Lys Pro Ser Ser Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser
 225 230 235 240

Thr Ser Thr Ser Thr Ser Thr Ser Ser Pro Pro Val Gln Pro
 245 250 255

Thr Thr Pro Ser Gly Cys Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly
 260 265 270

Asn Gly Trp Ser Gly Cys Thr Thr Cys Val Ala Gly Ser Thr Cys Thr
 275 280 285

Lys Ile Asn Asp Trp Tyr His Gln Cys Leu
 290 295

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1031 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 11..889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCATCCAAAC ATG CTT AAA ACG CTC GCT CCA TTG ATC ATC TTG GCC GCC
 Met Leu Lys Thr Leu Ala Pro Leu Ile Ile Leu Ala Ala
 300 305 310

49

TCG GTC ACA GCG CAA ACA GCA GGA GTT ACG ACC CGC TAC TGG GAC TGC Ser Val Thr Ala Gln Thr Ala Gly Val Thr Thr Arg Tyr Trp Asp Cys 315 320 325	97
TGC AAG CCA AGC TGT GGA TGG AGT GGA AAG GCT TCT GTT TCT GCT CCA Cys Lys Pro Ser Cys Gly Trp Ser Gly Lys Ala Ser Val Ser Ala Pro 330 335 340	145
GTC AGA ACT TGC GAT CGT AAT GGA AAT ACA CTT GGC CCA GAC GTG AAA Val Arg Thr Cys Asp Arg Asn Gly Asn Thr Leu Gly Pro Asp Val Lys 345 350 355	193
AGC GGA TGT GAT AGC GGT GGA ACG TCA TTC ACT TGC GCG AAC AAT GGT Ser Gly Cys Asp Ser Gly Gly Thr Ser Phe Thr Cys Ala Asn Asn Gly 360 365 370 375	241
CCA TTT GCG ATT GAC AAT AAC ACT GCA TAT GGT TTT GCT GCA GCC CAC Pro Phe Ala Ile Asp Asn Asn Thr Ala Tyr Gly Phe Ala Ala Ala His 380 385 390	289
TTA GCG GGC TCT AGC GAA GCA GCC TGG TGT TGC CAG TGC TAC GAA TTG Leu Ala Gly Ser Ser Glu Ala Ala Trp Cys Cys Gln Cys Tyr Glu Leu 395 400 405	337
ACG TTT ACG AGT GGA CCC GTA GTT GGG AAG AAA CTG ACC GTT CAA GTC Thr Phe Thr Ser Gly Pro Val Val Gly Lys Lys Leu Thr Val Gln Val 410 415 420	385
ACA AAC ACG GGA GGT GAC CTC GGA AAT AAT CAC TTT GAC CTG ATG ATC Thr Asn Thr Gly Gly Asp Leu Gly Asn Asn His Phe Asp Leu Met Ile 425 430 435	433
CCC GGT GGA GGT GTT GGC CTC TTC ACA CAA GGA TGT CCT GCT CAG TTT Pro Gly Gly Val Gly Leu Phe Thr Gln Gly Cys Pro Ala Gln Phe 440 445 450 455	481
GGG AGC TGG AAC GGG GGT GCT CAA TAC GGG GGT GTG TCC AGC CGT GAC Gly Ser Trp Asn Gly Gly Ala Gln Tyr Gly Gly Val Ser Ser Arg Asp 460 465 470	529
CAA TGC TCC CAA CTT CCA GCA GCT GTG CAA GCT GGA TGT CAA TTC CGT Gln Cys Ser Gln Leu Pro Ala Ala Val Gln Ala Gly Cys Gln Phe Arg 475 480 485	577
TTC GAC TGG ATG GGT GGC GCG GAT AAC CCC AAC GTC ACC TTC CGA CCT Phe Asp Trp Met Gly Gly Ala Asp Asn Pro Asn Val Thr Phe Arg Pro 490 495 500	625
GTG ACC TGC CCA GCG CAG CTC ACT AAT ATC TCG GGC TGT GTT CGT AAA Val Thr Cys Pro Ala Gln Leu Thr Asn Ile Ser Gly Cys Val Arg Lys 505 510 515	673
CCC TCC AGC AGC ACC AGC TCT CCG GTC AAC CAG CCT ACC AGC ACC AGC Pro Ser Ser Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr Ser 520 525 530 535	721

ACC ACG TCC ACC TCC ACC ACC TCG AGC CCG CCA GTC CAG CCT ACG ACT	769
Thr Thr Ser Thr Ser Thr Ser Pro Pro Val Gln Pro Thr Thr	
540 545 550	
CCC AGC GGC TGC ACT GCT GAG AGG TGG GCT CAG TGC GGC GGC AAT GGC	817
Pro Ser Gly Cys Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn Gly	
555 560 565	
TGG AGC GGC TGC ACC ACC TGC GTC GCT GGC AGC ACT TGC ACG AAG ATT	865
Trp Ser Gly Cys Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys Ile	
570 575 580	
AAT GAC TGG TAC CAT CAG TGC CTG TAGACGCAGG GCAGCTTGAG GCCCTTACTG	919
Asn Asp Trp Tyr His Gln Cys Leu	
585 590	
GTGGCGAAC GAAATGACAC TCCAATCAC TGTATTAGTT CTTGTACATA ATTCGTCAT	979
CCCTCCAGGG ATTGTCACAT AAATGCAATG AGGAACAATG AGTACAGAAT TC	1031

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Leu Lys Thr Leu Ala Pro Leu Ile Ile Leu Ala Ala Ser Val Thr	
1 5 10 15	
Ala Gln Thr Ala Gly Val Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro	
20 25 30	
Ser Cys Gly Trp Ser Gly Lys Ala Ser Val Ser Ala Pro Val Arg Thr	
35 40 45	
Cys Asp Arg Asn Gly Asn Thr Leu Gly Pro Asp Val Lys Ser Gly Cys	
50 55 60	
Asp Ser Gly Gly Thr Ser Phe Thr Cys Ala Asn Asn Gly Pro Phe Ala	
65 70 75 80	
Ile Asp Asn Asn Thr Ala Tyr Gly Phe Ala Ala Ala His Leu Ala Gly	
85 90 95	
Ser Ser Glu Ala Ala Trp Cys Cys Gln Cys Tyr Glu Leu Thr Phe Thr	
100 105 110	
Ser Gly Pro Val Val Gly Lys Lys Leu Thr Val Gln Val Thr Asn Thr	
115 120 125	

Gly Gly Asp Leu Gly Asn Asn His Phe Asp Leu Met Ile Pro Gly Gly
 130 135 140
 Gly Val Gly Leu Phe Thr Gln Gly Cys Pro Ala Gln Phe Gly Ser Trp
 145 150 155 160
 Asn Gly Gly Ala Gln Tyr Gly Val Ser Ser Arg Asp Gln Cys Ser
 165 170 175
 Gln Leu Pro Ala Ala Val Gln Ala Gly Cys Gln Phe Arg Phe Asp Trp
 180 185 190
 Met Gly Gly Ala Asp Asn Pro Asn Val Thr Phe Arg Pro Val Thr Cys
 195 200 205
 Pro Ala Gln Leu Thr Asn Ile Ser Gly Cys Val Arg Lys Pro Ser Ser
 210 215 220
 Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr Ser Thr Ser
 225 230 235 240
 Thr Ser Thr Thr Ser Ser Pro Pro Val Gln Pro Thr Thr Pro Ser Gly
 245 250 255
 Cys Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn Gly Trp Ser Gly
 260 265 270
 Cys Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys Ile Asn Asp Trp
 275 280 285
 Tyr His Gln Cys Leu
 290

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 42..971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAACAGTTCA AACACCTACA AGGTCCCGTG CCCTGTAGAC C ATG CGT TCC TCT	53
Met Arg Ser Ser	
295	
GCA GTC CTC ATC GGC CTC GTG GCC GGT GTG GCC GCC CAG TCC TCT GGC	101
Ala Val Leu Ile Gly Leu Val Ala Gly Val Ala Ala Gln Ser Ser Gly	
300 305 310	

ACC GGC CGC ACC ACC AGA TAC TGG GAC TGC TGC AAG CCG TCC TGC GGG		149
Thr Gly Arg Thr Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Gly		
315 320 325		
TGG GAC GAA AAG GCC TCC GTC AGC CAG CCC GTC AAG ACG TGC GAT AGG		197
Trp Asp Glu Lys Ala Ser Val Ser Gln Pro Val Lys Thr Cys Asp Arg		
330 335 340 345		
AAC AAC AAC CCT CTC GCG TCC ACG GCC AGG AGC GGC TGC GAT TCC AAC		245
Asn Asn Asn Pro Leu Ala Ser Thr Ala Arg Ser Gly Cys Asp Ser Asn		
350 355 360		
GGC GTC GCC TAC ACG TGC AAC GAT AAC CAG CCG TGG GCT GTC AAC GAT		293
Gly Val Ala Tyr Thr Cys Asn Asp Asn Gln Pro Trp Ala Val Asn Asp		
365 370 375		
AAC CTG GCC TAT GGT TTT GCT GCC ACG GCT TTC AGT GGT GGA TCG GAG		341
Asn Leu Ala Tyr Gly Phe Ala Ala Thr Ala Phe Ser Gly Gly Ser Glu		
380 385 390		
GCC AGC TGG TGC TGT GCC TGC TAT GCC CTT CAG TTC ACC TCC GGC CCT		389
Ala Ser Trp Cys Cys Ala Cys Tyr Ala Leu Gln Phe Thr Ser Gly Pro		
395 400 405		
GTT GCG GGA AAG ACC ATG GTC GTC CAG TCG ACA AAC ACC GGC GGC GAC		437
Val Ala Gly Lys Thr Met Val Val Gln Ser Thr Asn Thr Gly Gly Asp		
410 415 420 425		
CTC AGC GGC AAC CAC TTT GAC ATC CTC ATG CCC GGC GGC GGC CTG GGC		485
Leu Ser Gly Asn His Phe Asp Ile Leu Met Pro Gly Gly Gly Leu Gly		
430 435 440		
ATC TTC GAC GGC TGC ACC CCG CAA TGG GGC GTC AGC TTC CCC GGA AAC		533
Ile Phe Asp Gly Cys Thr Pro Gln Trp Gly Val Ser Phe Pro Gly Asn		
445 450 455		
CGC TAC GGC GGC ACC ACC AGC CGC AGC CAG TGC TCC CAA ATC CCC TCG		581
Arg Tyr Gly Thr Thr Ser Arg Ser Gln Cys Ser Gln Ile Pro Ser		
460 465 470		
GCC CTG CAG CCC GGC TGC AAC TGG CGG TAC GAC TGG TTC AAC GAC GCC		629
Ala Leu Gln Pro Gly Cys Asn Trp Arg Tyr Asp Trp Phe Asn Asp Ala		
475 480 485		
GAC AAC CCC GAC GTC TCG TGG CGC CGC GTC CAG TGC CCC GCC GCA CTC		677
Asp Asn Pro Asp Val Ser Trp Arg Arg Val Gln Cys Pro Ala Ala Leu		
490 495 500 505		
ACC GAC CGC ACC GGC TGC CGC CGC TCC GAT GAC GGG AAC TAT CCC GTC		725
Thr Asp Arg Thr Gly Cys Arg Arg Ser Asp Asp Gly Asn Tyr Pro Val		
510 515 520		
TTC CAG CCC GGT CCG CCC CCG GCC ACG ACG ATC AGG ACA TCG ACT ACC		773
Phe Gln Pro Gly Pro Pro Pro Ala Thr Thr Ile Arg Thr Ser Thr Thr		
525 530 535		

ATC ACA GCC TCA TCG TCG TCT TCG TCT TCG TCG TCG TCG ACT ACG GCT Ile Thr Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Thr Ala	821
540 545 550	
 GGT AGC CCG CCT GTG CCG ACT GGT GGT AGT GGG CCA ACG TCG CCT Gly Ser Pro Pro Val Pro Thr Gly Gly Ser Gly Pro Thr Ser Pro	869
555 560 565	
 GTC TGG GGA CAG TGC GGC GGT CAG GGA TGG AGT GGT CCT ACG CGT TGT Val Trp Gly Gln Cys Gly Gly Gln Gly Trp Ser Gly Pro Thr Arg Cys	917
570 575 580 585	
 GTT GCT GGG TCG ACA TGC AGT GTG GTC AAC CCG TGG TAC TCG CAG TGT Val Ala Gly Ser Thr Cys Ser Val Val Asn Pro Trp Tyr Ser Gln Cys	965
590 595 600	
 TTT CCT TAAGGAGCCT CTGGCTGAGC AGATCCTTTC GAAGAGGAGG GTCTCTGC Phe Pro	1021

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: protein
 - xii) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Arg	Ser	Ser	Ala	Val	Leu	Ile	Gly	Leu	Val	Ala	Gly	Val	Ala	Ala
1				5					10					15	
Gln	Ser	Ser	Gly	Thr	Gly	Arg	Thr	Thr	Arg	Tyr	Trp	Asp	Cys	Cys	Lys
				20				25					30		
Pro	Ser	Cys	Gly	Trp	Asp	Glu	Lys	Ala	Ser	Val	Ser	Gln	Pro	Val	Lys
				35				40					45		
Thr	Cys	Asp	Arg	Asn	Asn	Asn	Pro	Leu	Ala	Ser	Thr	Ala	Arg	Ser	Gly
				50			55					60			
Cys	Asp	Ser	Asn	Gly	Val	Ala	Tyr	Thr	Cys	Asn	Asp	Asn	Gln	Pro	Trp
				65			70			75				80	
Ala	Val	Asn	Asp	Asn	Leu	Ala	Tyr	Gly	Phe	Ala	Ala	Thr	Ala	Phe	Ser
				85					90					95	
Gly	Gly	Ser	Glu	Ala	Ser	Trp	Cys	Cys	Ala	Cys	Tyr	Ala	Leu	Gln	Phe
				100				105					110		

Thr	Ser	Gly	Pro	Val	Ala	Gly	Lys	Thr	Met	Val	Val	Gln	Ser	Thr	Asn
115															
120															125
<hr/>															
Thr	Gly	Gly	Asp	Leu	Ser	Gly	Asn	His	Phe	Asp	Ile	Leu	Met	Pro	Gly
130															140
Gly	Gly	Leu	Gly	Ile	Phe	Asp	Gly	Cys	Thr	Pro	Gln	Trp	Gly	Val	Ser
145															160
Phe	Pro	Gly	Asn	Arg	Tyr	Gly	Gly	Thr	Thr	Ser	Arg	Ser	Gln	Cys	Ser
165															175
170															
Gln	Ile	Pro	Ser	Ala	Leu	Gln	Pro	Gly	Cys	Asn	Trp	Arg	Tyr	Asp	Trp
180															190
Phe	Asn	Asp	Ala	Asp	Asn	Pro	Asp	Val	Ser	Trp	Arg	Arg	Val	Gln	Cys
195															205
Pro	Ala	Ala	Leu	Thr	Asp	Arg	Thr	Gly	Cys	Arg	Arg	Ser	Asp	Asp	Gly
210															220
Asn	Tyr	Pro	Val	Phe	Gln	Pro	Gly	Pro	Pro	Pro	Ala	Thr	Thr	Ile	Arg
225															240
Thr	Ser	Thr	Thr	Ile	Thr	Ala	Ser								
245															255
Ser	Thr	Thr	Ala	Gly	Ser	Pro	Pro	Val	Pro	Thr	Gly	Gly	Ser	Gly	
260															270
Pro	Thr	Ser	Pro	Val	Trp	Gly	Gln	Cys	Gly	Gly	Gln	Gly	Trp	Ser	Gly
275															285
Pro	Thr	Arg	Cys	Val	Ala	Gly	Ser	Thr	Cys	Ser	Val	Val	Asn	Pro	Trp
290															300
Tyr	Ser	Gln	Cys	Phe	Pro										
305															310

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG	TTC	TCT	CCG	CTC	TGG	GCC	CTG	TCG	GCT	CTG	CTC	CTA	TTT	CCT	GCC	48
Met	Phe	Ser	Pro	Leu	Trp	Ala	Leu	Ser	Ala	Leu	Leu	Leu	Phe	Pro	Ala	
315							320						325			
ACT	GAA	GCC	ACT	AGC	GGC	GTG	ACA	ACC	AGG	TAC	TGG	GAC	TGC	TGC	AAG	96
Thr	Glu	Ala	Thr	Ser	Gly	Val	Thr	Thr	Arg	Tyr	Trp	Asp	Cys	Cys	Lys	
330				335					340							
CCG	TCT	TGT	GCT	TGG	ACG	GGC	AAA	GCA	TCC	GTC	TCC	AAG	CCC	GTC	GGA	144
Pro	Ser	Cys	Ala	Trp	Thr	Gly	Lys	Ala	Ser	Val	Ser	Lys	Pro	Val	Gly	
345				350					355							
ACC	TGC	GAC	ATC	AAC	GAC	AAC	GCC	CAG	ACG	CCG	AGC	GAT	CTG	CTC	AAG	192
Thr	Cys	Asp	Ile	Asn	Asp	Asn	Ala	Gln	Thr	Pro	Ser	Asp	Leu	Leu	Lys	
360				365					370							
TCG	TCC	TGT	GAT	GGC	GGC	AGC	GCC	TAC	TAC	TGC	AGC	AAC	CAG	GGC	CCA	240
Ser	Ser	Cys	Asp	Gly	Gly	Ser	Ala	Tyr	Tyr	Cys	Ser	Asn	Gln	Gly	Pro	
375				380				385					390			
TGG	GCC	GTG	AAC	GAC	AGC	CTT	TCC	TAC	GGC	TTC	GCT	GCC	GCC	AAG	CTG	288
Trp	Ala	Val	Asn	Asp	Ser	Leu	Ser	Tyr	Gly	Phe	Ala	Ala	Ala	Lys	Leu	
						395		400			405					
TCC	GGA	AAG	CAG	GAG	ACT	GAT	TGG	TGC	TGT	GGC	TGC	TAC	AAG	CTC	ACA	336
Ser	Gly	Lys	Gln	Glu	Thr	Asp	Trp	Cys	Cys	Gly	Cys	Tyr	Lys	Leu	Thr	
410				415							420					
TTC	ACC	TCC	ACC	GCC	GTT	TCC	GGC	AAG	CAA	ATG	ATC	GTG	CAA	ATC	ACG	384
Phe	Thr	Ser	Thr	Ala	Val	Ser	Gly	Lys	Gln	Met	Ile	Val	Gln	Ile	Thr	
425						430					435					
AAC	ACG	GGC	GGC	GAC	CTC	GGC	AAC	AAC	CAC	TTC	GAC	ATC	GCC	ATG	CCG	432
Asn	Thr	Gly	Gly	Asp	Leu	Gly	Asn	Asn	His	Phe	Asp	Ile	Ala	Met	Pro	
440				445						450						
GGC	GGC	GGC	GTC	GGC	ATC	TTC	AAC	GGG	TGC	TCC	AAG	CAA	TGG	AAC	GGC	480
Gly	Gly	Gly	Val	Gly	Ile	Phe	Asn	Gly	Cys	Ser	Lys	Gln	Trp	Asn	Gly	
455				460				465					470			
ATC	AAT	CTG	GGC	AAC	CAG	TAT	GGC	GGC	TTC	ACT	GAC	CGC	TCG	CAA	TGT	528
Ile	Asn	Leu	Gly	Asn	Gln	Tyr	Gly	Gly	Phe	Thr	Asp	Arg	Ser	Gln	Cys	
						475		480			485					
GCG	ACG	CTC	CCG	TCC	AAG	TGG	CAG	GCC	AGC	TGC	AAC	TGG	CGC	TTC	GAC	576
Ala	Thr	Leu	Pro	Ser	Lys	Trp	Gln	Ala	Ser	Cys	Asn	Trp	Arg	Phe	Asp	
490						495					500					
TGG	TTC	GAG	AAT	GCC	GAC	AAC	CCC	ACC	GTC	GAT	TGG	GAG	CCT	GTC	ACT	624
Trp	Phe	Glu	Asn	Ala	Asp	Asn	Pro	Thr	Val	Asp	Trp	Glu	Pro	Val	Thr	
						505		510			515					
TGC	CCA	CAG	GAA	TTG	GTC	GCC	CGG	ACT	GGC	TGT	TCC	CGT	ACC	CCC	TCC	672
Cys	Pro	Gln	Glu	Leu	Val	Ala	Arg	Thr	Gly	Cys	Ser	Arg	Thr	Pro	Ser	
520						525					530					

AGC AGC ACC AGC TCT CCG GTC AAC CAG CCT ACC AGC ACC AGC ACC ACG	720
Ser Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr Ser Thr Thr	
535 540 545 550	
TCC ACC TCC ACC ACC TCG AGC CCG CCA GTC CAG CCT ACG ACT CCC AGC	768
Ser Thr Ser Thr Ser Ser Pro Pro Val Gln Pro Thr Thr Pro Ser	
555 560 565	
GGC TGC ACT GCT GAG AGG TGG GCT CAG TGC GGC GGC AAT GGC TGG AGC	816
Gly Cys Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn Gly Trp Ser	
570 575 580	
GGC TGC ACC ACC TGC GTC GCT GGC AGC ACT TGC ACG AAG ATT AAT GAC	864
Gly Cys Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys Ile Asn Asp	
585 590 595	
TGG TAC CAT CAG TGC CTG TAG	885
Trp Tyr His Gln Cys Leu	
600	

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: protein
 - xii) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Phe	Ser	Pro	Leu	Trp	Ala	Leu	Ser	Ala	Leu	Leu	Leu	Phe	Pro	Ala
1				5						10					15
Thr	Glu	Ala	Thr	Ser	Gly	Val	Thr	Thr	Arg	Tyr	Trp	Asp	Cys	Cys	Lys
						20					25				30
Pro	Ser	Cys	Ala	Trp	Thr	Gly	Lys	Ala	Ser	Val	Ser	Lys	Pro	Val	Gly
							35			40					45
Thr	Cys	Asp	Ile	Asn	Asp	Asn	Ala	Gln	Thr	Pro	Ser	Asp	Leu	Leu	Lys
							50			55					60
Ser	Ser	Cys	Asp	Gly	Gly	Ser	Ala	Tyr	Tyr	Cys	Ser	Asn	Gln	Gly	Pro
							65			70					80
Trp	Ala	Val	Asn	Asp	Ser	Leu	Ser	Tyr	Gly	Phe	Ala	Ala	Ala	Lys	Leu
							85			90					95
Ser	Gly	Lys	Gln	Glu	Thr	Asp	Trp	Cys	Cys	Gly	Cys	Tyr	Lys	Leu	Thr
								100			105				110
Phe	Thr	Ser	Thr	Ala	Val	Ser	Gly	Lys	Gln	Met	Ile	Val	Gln	Ile	Thr
										115					125
										120					

Asn	Thr	Gly	Gly	Asp	Leu	Gly	Asn	Asn	His	Phe	Asp	Ile	Ala	Met	Pro
130							135				140				
Gly	Gly	Gly	Val	Gly	Ile	Phe	Asn	Gly	Cys	Ser	Lys	Gln	Trp	Asn	Gly
145							150			155				160	
Ile	Asn	Leu	Gly	Asn	Gln	Tyr	Gly	Gly	Phe	Thr	Asp	Arg	Ser	Gln	Cys
						165			170				175		
Ala	Thr	Leu	Pro	Ser	Lys	Trp	Gln	Ala	Ser	Cys	Asn	Trp	Arg	Phe	Asp
						180			185			190			
Trp	Phe	Glu	Asn	Ala	Asp	Asn	Pro	Thr	Val	Asp	Trp	Glu	Pro	Val	Thr
						195			200			205			
Cys	Pro	Gln	Glu	Leu	Val	Ala	Arg	Thr	Gly	Cys	Ser	Arg	Thr	Pro	Ser
						210			215			220			
Ser	Ser	Thr	Ser	Ser	Pro	Val	Asn	Gln	Pro	Thr	Ser	Thr	Ser	Thr	Thr
						225			230			235			240
Ser	Thr	Ser	Thr	Ser	Ser	Pro	Pro	Val	Gln	Pro	Thr	Thr	Pro	Ser	
						245			250			255			
Gly	Cys	Thr	Ala	Glu	Arg	Trp	Ala	Gln	Cys	Gly	Gly	Asn	Gly	Trp	Ser
						260			265			270			
Gly	Cys	Thr	Thr	Cys	Val	Ala	Gly	Ser	Thr	Cys	Thr	Lys	Ile	Asn	Asp
						275			280			285			
Trp	Tyr	His	Gln	Cys	Leu										
						290									

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAAGATACAA	T	ATG	CGT	TCC	TCC	ACT	ATT	TTG	CAA	ACC	GGC	CTG	GTG	GCC	
		Met	Arg	Ser	Ser	Thr	Ile	Leu	Gln	Thr	Gly	Leu	Val	Ala	50
								300					305		

GTT	CTC	CCC	TTC	GCC	GTC	CAG	GCC	GCC	TCA	GGA	TCC	GGC	AAG	TCC	ACC	
Val	Leu	Pro	Phe	Ala	Val	Gln	Ala	Ala	Ser	Gly	Ser	Gly	Lys	Ser	Thr	98
								315				320				

AGA TAT TGG GAC TGC TGC AAA CCA TCT TGT GCC TGG TCC GGC AAG GCT Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp Ser Gly Lys Ala	325	330	335	146
TCT GTC AAC CGC CCT GTT CTC GCC TGC AAC GCA AAC AAC AAC CCG CTG Ser Val Asn Arg Pro Val Leu Ala Cys Asn Ala Asn Asn Asn Pro Leu	340	345	350	355
AAC GAC GCC AAC GTC AAG TCA GGA TGT GAT GGC GGT TCT GCA TAC ACC Asn Asp Ala Asn Val Lys Ser Gly Cys Asp Gly Gly Ser Ala Tyr Thr	360	365	370	194
TGT GCC AAC AAC TCT CCC TGG GCA GTG AAT GAC AAT CTG GCC TAC GGC Cys Ala Asn Asn Ser Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly	375	380	385	242
TTC GCG GCC ACA AAA CTC AGC GGG GGG ACC GAG TCA TCT TGG TGC TGC Phe Ala Ala Thr Lys Leu Ser Gly Gly Thr Glu Ser Ser Trp Cys Cys	390	395	400	338
GCC TGT TAT GCC CTC ACA TTC ACA TCG GGT CCT GTT TCT GGC AAA ACC Ala Cys Tyr Ala Leu Thr Phe Thr Ser Gly Pro Val Ser Gly Lys Thr	405	410	415	290
TTG GTT GTC CAG TCT ACC AGT ACC GGT GGT GAT CTT GGC Leu Val Val Gln Ser Thr Ser Thr Gly Gly Asp Leu Gly	420	425	430	425

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: protein
 - xii) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Met Arg Ser Ser Thr Ile Leu Gln Thr Gly Leu Val Ala Val Leu Pro
1 5 10 15

Phe Ala Val Gln Ala Ala Ser Gly Ser Gly Lys Ser Thr Arg Tyr Trp
20 25 30

Asp Cys Cys Lys Pro Ser Cys Ala Trp Ser Gly Lys Ala Ser Val Asn
35 40 45

Arg Pro Val Leu Ala Cys Asn Ala Asn Asn Asn Pro Leu Asn Asp Ala
50 55 60

Asn Val Lys Ser Gly Cys Asp Gly Gly Ser Ala Tyr Thr Cys Ala Asn
65 70 75 80

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Asn Ser Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala
85 90 95

Thr Lys Leu Ser Gly Gly Thr Glu Ser Ser Trp Cys Cys Ala Cys Tyr
100 105 110

Ala Leu Thr Phe Thr Ser Gly Pro Val Ser Gly Lys Thr Leu Val Val
115 120 125

Gln Ser Thr Ser Thr Gly Gly Asp Leu Gly
130 135

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCG GCT TGC GAT AAC GGT GGT GGC ACT GCA TAC ATG TGT GCC AGC CAG 48
Ser Ala Cys Asp Asn Gly Gly Thr Ala Tyr Met Cys Ala Ser Gln
140 145 150

GAG CCG TGG GCA GTG AGC TCC AAC GTC GCG TAC GGC TTT GCT GCA GTT 96
Glu Pro Trp Ala Val Ser Ser Asn Val Ala Tyr Gly Phe Ala Ala Val
155 160 165 170

AGA ATC AGC GGA 108
Arg Ile Ser Gly

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Ala Cys Asp Asn Gly Gly Thr Ala Tyr Met Cys Ala Ser Gln
1 5 10 15

Glu Pro Trp Ala Val Ser Ser Asn Val Ala Tyr Gly Phe Ala Ala Val
20 25 30

Arg Ile Ser Gly
35

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCC TGC AAC GCA AAC TTC CAG CGC ATC AGT GAC CCC AAC GCC AAG TCG 48
Ala Cys Asn Ala Asn Phe Gln Arg Ile Ser Asp Pro Asn Ala Lys Ser
40 45 50

GGC TGC GAT GGT GGC TCG GCC TTC TCT TGC GCC AAA CAA ACC CCT TGG 96
Gly Cys Asp Gly Gly Ser Ala Phe Ser Cys Ala Lys Gln Thr Pro Trp
55 60 65

GCC 99
Ala

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ala Cys Asn Ala Asn Phe Gln Arg Ile Ser Asp Pro Asn Ala Lys Ser
1 5 10 15

Gly Cys Asp Gly Gly Ser Ala Phe Ser Cys Ala Lys Gln Thr Pro Trp
20 25 30

Ala

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAC CAG CCG CTC GGC GGA CAA CGG ACG CGA CCA AGG AGC GCG TGC GAC	48		
Asp Gln Pro Leu Gly Gly Gln Arg Thr Arg Pro Arg Ser Ala Cys Asp			
35	40	45	
AAT GGC GGC TCT GCA TAC ATG TGC AGC AAC CAG AGC CCG TGG GCC GTC	96		
Asn Gly Gly Ser Ala Tyr Met Cys Ser Asn Gln Ser Pro Trp Ala Val			
50	55	60	65
GAC GAT TCT CTC AGT TAC GGA TGG GCT GCC GTT AGG ATC TAT GGA CAT	144		
Asp Asp Ser Leu Ser Tyr Gly Trp Ala Ala Val Arg Ile Tyr Gly His			
70	75	80	
ACC GAA ACT ACT TGG TGC TGC GCT TGC TAC GAG TTG ACT TTT ACC AGC	192		
Thr Glu Thr Thr Trp Cys Cys Ala Cys Tyr Glu Leu Thr Phe Thr Ser			
85	90	95	
GGT CCG GTT AGC GGC AAG AAG ATG ATT GTT CAG	225		
Gly Pro Val Ser Gly Lys Lys Met Ile Val Gln			
100	105		

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asp Gln Pro Leu Gly Gly Gln Arg Thr Arg Pro Arg Ser Ala Cys Asp			
1	5	10	15
Asn Gly Gly Ser Ala Tyr Met Cys Ser Asn Gln Ser Pro Trp Ala Val			
20	25	30	
Asp Asp Ser Leu Ser Tyr Gly Trp Ala Ala Val Arg Ile Tyr Gly His			
35	40	45	

Thr Glu Thr Thr Trp Cys Cys Ala Cys Tyr Glu Leu Thr Phe Thr Ser
50 55 60

Gly Pro Val Ser Gly Lys Lys Met Ile Val Gln
65 70 75

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGA AAC GAC AAC CCC ATC TCC AAC ACC AAC GCT GTC AAC GGT TGT GAG	48
Arg Asn Asp Asn Pro Ile Ser Asn Thr Asn Ala Val Asn Gly Cys Glu	
80 85 90	
GGT GGT GGT TCT GCT TAT GCT TGC ACC AAC TAC TCT CCC TGG GCT GTC	96
Gly Gly Ser Ala Tyr Ala Cys Thr Asn Tyr Ser Pro Trp Ala Val	
95 100 105	
AAC GAT GAG CTT GCC TAC GGT TTC GCT GCT ACC AAG ATC TCC GGT GGC	144
Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala Thr Lys Ile Ser Gly Gly	
110 115 120	
TCC GAG GCC AGC TGG TGC TGT GCC TGC TAT CTA	177
Ser Glu Ala Ser Trp Cys Cys Ala Cys Tyr Leu	
125 130	

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg Asn Asp Asn Pro Ile Ser Asn Thr Asn Ala Val Asn Gly Cys Glu	
1 5 10 15	
Gly Gly Ser Ala Tyr Ala Cys Thr Asn Tyr Ser Pro Trp Ala Val	
20 25 30	

Asn Asp Glu Leu Ala Tyr Gly Phe Ala Ala Thr Lys Ile Ser Gly Gly
35 40 45

Ser Glu Ala Ser Trp Cys Cys Ala Cys Tyr Leu
50 55

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGC GGC TGT GAC GGT GGT TCT GCC TAC GCC TGT GCA AAC AAC TCC CCT 48
Ser Gly Cys Asp Gly Gly Ser Ala Tyr Ala Cys Ala Asn Asn Ser Pro
60 65 70 75

TGG GCT GTC AAC GAT 63
Trp Ala Val Asn Asp
80

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Gly Cys Asp Gly Gly Ser Ala Tyr Ala Cys Ala Asn Asn Ser Pro
1 5 10 15

Trp Ala Val Asn Asp
20

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAC CAG CCT GTC TTC ACT TGC GAC GCC AAA TTC CAG CGC ATC ACC GAC	48	
Asn Gln Pro Val Phe Thr Cys Asp Ala Lys Phe Gln Arg Ile Thr Asp		
25	30	35
CCC AAT ACC AAG TCG GGC TGC GAT GGC GGC TCG GCC TTT TCG TGT GCT	96	
Pro Asn Thr Lys Ser Gly Cys Asp Gly Ser Ala Phe Ser Cys Ala		
40	45	50
GAC CAA ACC CCC TGG GCT CTG AAC GAC GAT TTC GCC TAT GGC TTC GCT	144	
Asp Gln Thr Pro Trp Ala Leu Asn Asp Asp Phe Ala Tyr Gly Phe Ala		
55	60	65
GCC ACG GCT ATT TCG GGT GGA TCG GAA GCC TCG	177	
Ala Thr Ala Ile Ser Gly Gly Ser Glu Ala Ser		
70	75	80

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asn Gln Pro Val Phe Thr Cys Asp Ala Lys Phe Gln Arg Ile Thr Asp			
1	5	10	15
Pro Asn Thr Lys Ser Gly Cys Asp Gly Ser Ala Phe Ser Cys Ala			
20	25	30	
Asp Gln Thr Pro Trp Ala Leu Asn Asp Asp Phe Ala Tyr Gly Phe Ala			
35	40	45	
Ala Thr Ala Ile Ser Gly Gly Ser Glu Ala Ser			
50	55		

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTC TAC GCC TGC AAC GCA AAC TTC CAG CGC ATC ACC GAC GCC AAC GCC	48		
Val Tyr Ala Cys Asn Ala Asn Phe Gln Arg Ile Thr Asp Ala Asn Ala			
60	65	70	75
AAG TCC GGC TGC GAT GGC GGC TCC GCC TTC TCG TGC GCC AAC CAG ACC	96		
Lys Ser Gly Cys Asp Gly Ser Ala Phe Ser Cys Ala Asn Gln Thr			
80	85	90	
CCG TGG GCC GTG AGC GAC GAC TTT GCC TAC GGT TTC GCG GCT ACG GCG	144		
Pro Trp Ala Val Ser Asp Asp Phe Ala Tyr Gly Phe Ala Ala Thr Ala			
95	100	105	
CTC GCC GGC	153		
Leu Ala Gly			
110			

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Val Tyr Ala Cys Asn Ala Asn Phe Gln Arg Ile Thr Asp Ala Asn Ala			
1	5	10	15
Lys Ser Gly Cys Asp Gly Ser Ala Phe Ser Cys Ala Asn Gln Thr			
20	25	30	
Pro Trp Ala Val Ser Asp Asp Phe Ala Tyr Gly Phe Ala Ala Thr Ala			
35	40	45	
Leu Ala Gly			
50			

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTC AAC CGC CCT GTC CTC GCC TGC GAC GCA AAC AAC AAC CCT CTG ACC	48
Val Asn Arg Pro Val Leu Ala Cys Asp Ala Asn Asn Asn Pro Leu Thr	
55 60 65	
GAC GCC GGC GTC AAG TCC GGA TGT GAT GGC GGT TCT GCA TAC ACC TGT	96
Asp Ala Gly Val Lys Ser Gly Cys Asp Gly Ser Ala Tyr Thr Cys	
70 75 80	
GCC AAC AAC TCC CCA TGG GCA GTG AAC GAC CAG CTC GCC TAC GGC TTT	144
Ala Asn Asn Ser Pro Trp Ala Val Asn Asp Gln Leu Ala Tyr Gly Phe	
85 90 95	
GCC GCC ACC AAA CTG AGC GGC GGA ACT GAG TCG TCA	180
Ala Ala Thr Lys Leu Ser Gly Gly Thr Glu Ser Ser	
100 105 110	

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Val Asn Arg Pro Val Leu Ala Cys Asp Ala Asn Asn Asn Pro Leu Thr	
1 5 10 15	
Asp Ala Gly Val Lys Ser Gly Cys Asp Gly Ser Ala Tyr Thr Cys	
20 25 30	
Ala Asn Asn Ser Pro Trp Ala Val Asn Asp Gln Leu Ala Tyr Gly Phe	
35 40 45	
Ala Ala Thr Lys Leu Ser Gly Gly Thr Glu Ser Ser	
50 55 60	

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGC TGC GAC GGC GGC AGC GCC TTC ACC TGC TCC AAC AAC TCT CCA TGG	48	
Gly Cys Asp Gly Gly Ser Ala Phe Thr Cys Ser Asn Asn Ser Pro Trp		
65	70	75
GCT GTG AAC GAA GAT	63	
Ala Val Asn Glu Asp		
80		

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Gly Cys Asp Gly Gly Ser Ala Phe Thr Cys Ser Asn Asn Ser Pro Trp			
1	5	10	15
Ala Val Asn Glu Asp			
20			

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACA AGA AAC GAC GGG CCC CTG TCC AGC CCC GAT GCC GCC TCC GGC TGT	48	
Thr Arg Asn Asp Gly Pro Leu Ser Ser Pro Asp Ala Ala Ser Gly Cys		
25	30	35

GAT GGC GGC GAA GCC TTT GCC TGT TCT AAT ACC TCG CCT TGG GCC GTC	96	
Asp Gly Gly Glu Ala Phe Ala Cys Ser Asn Thr Ser Pro Trp Ala Val		
40	45	50
AGC GAC CAG CTC GCG TAC GGA TAC GTC GCC ACG TCC ATC TCC GGC GGC	144	
Ser Asp Gln Leu Ala Tyr Gly Tyr Val Ala Thr Ser Ile Ser Gly Gly		
55	60	65
ACC GAG TCA		153
Thr Glu Ser		
70		

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Thr Arg Asn Asp Gly Pro Leu Ser Ser Pro Asp Ala Ala Ser Gly Cys			
1	5	10	15
Asp Gly Gly Glu Ala Phe Ala Cys Ser Asn Thr Ser Pro Trp Ala Val			
20	25	30	
Ser Asp Gln Leu Ala Tyr Gly Tyr Val Ala Thr Ser Ile Ser Gly Gly			
35	40	45	
Thr Glu Ser			
50			

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..159
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTC CGA ACG TGT AGT GCC AAC GAC TCG CCC TTG TCC GAC CCA AAT GCC	48	
Val Arg Thr Cys Ser Ala Asn Asp Ser Pro Leu Ser Asp Pro Asn Ala		
55	60	65

CCA AGT GGG TGT GAC GGT GGT AGC GCC TTC ACT TGT TCC AAC AAC TCC	96	
Pro Ser Gly Cys Asp Gly Gly Ser Ala Phe Thr Cys Ser Asn Asn Ser		
70	75	80
CCG TGG GCA GTC GAT GAC CAG ACA GCT TAT GGC TTT GCG GCA ACA GCC	144	
Pro Trp Ala Val Asp Asp Gln Thr Ala Tyr Gly Phe Ala Ala Thr Ala		
85	90	95
ATC AGT GGC CAG TCC	159	
Ile Ser Gly Gln Ser		
100		

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Val Arg Thr Cys Ser Ala Asn Asp Ser Pro Leu Ser Asp Pro Asn Ala			
1	5	10	15
Pro Ser Gly Cys Asp Gly Gly Ser Ala Phe Thr Cys Ser Asn Asn Ser			
20	25	30	
Pro Trp Ala Val Asp Asp Gln Thr Ala Tyr Gly Phe Ala Ala Thr Ala			
35	40	45	
Ile Ser Gly Gln Ser			
50			

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TGT GAG AAG AAC GAC AAC CCC TTA GCT GAC TTC AGC ACG AAA TCC GGG	48	
Cys Glu Lys Asn Asp Asn Pro Leu Ala Asp Phe Ser Thr Lys Ser Gly		
55	60	65

TGT GAA AGC GGA GGT TCG GCT TAT ACG TGT AAC AAC CAA TCA CCA TGG	96
Cys Glu Ser Gly Gly Ser Ala Tyr Thr Cys Asn Asn Gln Ser Pro Trp	
70 75 80 85	
GCC GTC AAT GAC TTG GTG TCG TAT GGC TTC GCC GCC ACA GCG ATC AAT	144
Ala Val Asn Asp Leu Val Ser Tyr Gly Phe Ala Ala Thr Ala Ile Asn	
90 95 100	
GGT GGC AAT	153
Gly Gly Asn	

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

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Cys Glu Lys Asn Asp Asn Pro Leu Ala Asp Phe Ser Thr Lys Ser Gly
1 5 10 15

Cys Glu Ser Gly Gly Ser Ala Tyr Thr Cys Asn Asn Gln Ser Pro Trp
20 25 30

Ala Val Asn Asp Leu Val Ser Tyr Gly Phe Ala Ala Thr Ala Ile Asn
35 40 45

Gly Gly Asn
50

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(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..171
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGC CGC CCC GTC GGA ACC TGC AAG AGG AAC GAC AAC CCC CTC TCC GAC
 Ser Arg Pro Val Gly Thr Cys Lys Arg Asn Asp Asn Pro Leu Ser Asp
 55 60 65

CCC GAT GCC AAG TCC GGC TGC GAC GGC GGC GGC GCC TTC ATG TGC TCC	96	
Pro Asp Ala Lys Ser Gly Cys Asp Gly Gly Ala Phe Met Cys Ser		
70	75	80
ACC CAG CAG CCG TGG GCC GTC AAC GAC AAT CTG GCA TAT GGC TTC GCC	144	
Thr Gln Gln Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Phe Ala		
85	90	95
GCC ACG GCC ATC AGC GGC GGC AAC GAG	171	
Ala Thr Ala Ile Ser Gly Gly Asn Glu		
100	105	

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Arg Pro Val Gly Thr Cys Lys Arg Asn Asp Asn Pro Leu Ser Asp			
1	5	10	15
Pro Asp Ala Lys Ser Gly Cys Asp Gly Gly Ala Phe Met Cys Ser			
20	25	30	
Thr Gln Gln Pro Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala			
35	40	45	
Ala Thr Ala Ile Ser Gly Gly Asn Glu			
50	55		

(2) INFORMATION FOR SEQ ID NO:53::

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACT TGC AAC AAG AAC GAC GGG CCC CTG TCC AGC CCC GAT GCC GCC TCC	48	
Thr Cys Asn Lys Asn Asp Gly Pro Leu Ser Ser Pro Asp Ala Ala Ser		
60	65	70

GCC TGT GAT GGC GGC GAA GCC TTT GCC TGT TCT AAT ACC TCG CCT TGG 96
Gly Cys Asp Gly Gly Glu Ala Phe Ala Cys Ser Asn Thr Ser Pro Trp
75 80 85

GCC GTC AGC GAC CAG CTC GCG TAC GGA TAC CTC GCC ACG TCC ATC TCC 144
Ala Val Ser Asp Gln Leu Ala Tyr Gly Tyr Leu Ala Thr Ser Ile Ser
90 95 100 105

GGC GGC ACC GAG TCG 159
Gly Gly Thr Glu Ser
110

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Thr Cys Asn Lys Asn Asp Gly Pro Leu Ser Ser Pro Asp Ala Ala Ser
1 5 10 15

Gly Cys Asp Gly Gly Glu Ala Phe Ala Cys Ser Asn Thr Ser Pro Trp
20 25 30

Ala Val Ser Asp Gln Leu Ala Tyr Gly Tyr Leu Ala Thr Ser Ile Ser
35 40 45

Gly Gly Thr Glu Ser
50

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CCA GTT TTC TCC TGT GAC AAG TAC GAC AAC CCT CTA CCT GAC GCC AAT 48
Pro Val Phe Ser Cys Asp Lys Tyr Asp Asn Pro Leu Pro Asp Ala Asn
55 60 65

GCT GTG TCC GGG TGT GAC CCC GGA GGT ACT GCC TTC
Ala Val Ser Gly Cys Asp Pro Gly Gly Thr Ala Phe
70 75 80

84

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Pro Val Phe Ser Cys Asp Lys Tyr Asp Asn Pro Leu Pro Asp Ala Asn
1 5 10 15

Ala Val Ser Gly Cys Asp Pro Gly Gly Thr Ala Phe
20 25

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACC TGC GAC GCC TGC GAC AGC CCC CTC AGC GAC TAC GAC GCC AAG TCC
Thr Cys Asp Ala Cys Asp Ser Pro Leu Ser Asp Tyr Asp Ala Lys Ser
30 35 40

48

GGC TGC GAC GGC GGT AGC GCA TAC ACC TGC ACC TAC TCT ACC CCC TGG
Gly Cys Asp Gly Gly Ser Ala Tyr Thr Cys Thr Tyr Ser Thr Pro Trp
45 50 55 60

96

GCC GTC GAC GAC AAC CTC TCC TAC GGT TTC GCC GCC AAG CTG AGC
Ala Val Asp Asp Asn Leu Ser Tyr Gly Phe Ala Ala Ala Lys Leu Ser
65 70 75

144

GGA
Gly

147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Thr Cys Asp Ala Cys Asp Ser Pro Leu Ser Asp Tyr Asp Ala Lys Ser
1 5 10 15

Gly Cys Asp Gly Gly Ser Ala Tyr Thr Cys Thr Tyr Ser Thr Pro Trp
20 25 30

Ala Val Asp Asp Asn Leu Ser Tyr Gly Phe Ala Ala Ala Lys Leu Ser
35 40 45

Gly

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCA CTA GCA GAT TTC ACC GGT GGA ACC GGC TGT AAT GGC GGT TCG ACA 48
Pro Leu Ala Asp Phe Thr Gly Gly Thr Gly Cys Asn Gly Ser Thr
50 55 60 65

TTC TCA TGC TCA AAC CAA CAA CCA TGG GCG GTC AAC GAC ACA TTC TCG 96
Phe Ser Cys Ser Asn Gln Gln Pro Trp Ala Val Asn Asp Thr Phe Ser
70 75 80

TAC GGC TTT GCG GGC ATC TTT ATC ACA GGC CAT GTC GAG 135
Tyr Gly Phe Ala Gly Ile Phe Ile Thr Gly His Val Glu
85 90

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Pro Leu Ala Asp Phe Thr Gly Gly Thr Gly Cys Asn Gly Gly Ser Thr
1 5 10 15

Phe Ser Cys Ser Asn Gln Gln Pro Trp Ala Val Asn Asp Thr Phe Ser
20 25 30

Tyr Gly Phe Ala Gly Ile Phe Ile Thr Gly His Val Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GCC AAA TCT GGA TGT GAT GCT GGT GGA GGT CAA GCC TAC ATG TGC TCC 48
Ala Lys Ser Gly Cys Asp Ala Gly Gly Gln Ala Tyr Met Cys Ser
50 55 60

AAC CAA CAA CCT TGG GTA GTC AAC GAC AAC CTC GCC TAC GGT TTC GCC 96
Asn Gln Gln Pro Trp Val Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala
65 70 75

GCA GTC AAC ATT GCC GGC 114
Ala Val Asn Ile Ala Gly
80

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Ala Lys Ser Gly Cys Asp Ala Gly Gly Gln Ala Tyr Met Cys Ser
 1 5 10 15
 Asn Gln Gln Pro Trp Val Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala
 20 25 30
 Ala Val Asn Ile Ala Gly
 35

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

T TCG ACG TCC GGG TGC GAC AAT GGC GGC AGC GCC TTC ATG TGC TCT	46
Ser Thr Ser Gly Cys Asp Asn Gly Gly Ser Ala Phe Met Cys Ser	
40 45 50	
AAC CAA AGC CCC TGG GCC GTC AAC GAC GAT CTG GCC TAC GGC TGG GCC	94
Asn Gln Ser Pro Trp Ala Val Asn Asp Asp Leu Ala Tyr Gly Trp Ala	
55 60 65	
GCC GTC TCA ATC GCG GGC C	113
Ala Val Ser Ile Ala Gly	
70 75	

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ser Thr Ser Gly Cys Asp Asn Gly Gly Ser Ala Phe Met Cys Ser Asn	
1 5 10 15	
Gln Ser Pro Trp Ala Val Asn Asp Asp Leu Ala Tyr Gly Trp Ala Ala	
20 25 30	

Val Ser Ile Ala Gly
35

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCA ACA CCG GTG CAG ACG TGC GAC CGC AAC GAC AAC CCG CTC TAC GAC	48	
Ser Thr Pro Val Gln Thr Cys Asp Arg Asn Asn Pro Leu Tyr Asp		
40	45	50

GGC GGG TCG ACG CCG TCC GGC TGC GAC GCC GGC GGC GCC TAC ATG	96	
Gly Gly Ser Thr Arg Ser Gly Cys Asp Ala Gly Gly Ala Tyr Met		
55	60	65

TGC TCG TCG CAC AGC CCG TGG GCC GTC AGC GAC AGC CTC TCG TAC GGC	144		
Cys Ser Ser His Ser Pro Trp Ala Val Ser Asp Ser Leu Ser Tyr Gly			
70	75	80	85

TGG GCG GCC GTC CGC ATC GCC GGC CAG TCC GAG	177
Trp Ala Ala Val Arg Ile Ala Gly Gln Ser Glu	
90	95

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ser Thr Pro Val Gln Thr Cys Asp Arg Asn Asp Asn Pro Leu Tyr Asp			
1	5	10	15

Gly Gly Ser Thr Arg Ser Gly Cys Asp Ala Gly Gly Ala Tyr Met		
20	25	30

Cys Ser Ser His Ser Pro Trp Ala Val Ser Asp Ser Leu Ser Tyr Gly		
35	40	45

Trp Ala Ala Val Arg Ile Ala Gly Gln Ser Glu
50 55

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

AAC GAC AAC CCC ATC TCC AAC ACC AAC GCT GTC AAC GGT TGT GAG GGT	48
Asn Asp Asn Pro Ile Ser Asn Thr Asn Ala Val Asn Gly Cys Glu Gly	
60 65 70 75	
GGT GGT TCT GCT TAC GCT TGC TCC AAC TAC TCT CCC TGG GCT GTC AAC	96
Gly Gly Ser Ala Tyr Ala Cys Ser Asn Tyr Ser Pro Trp Ala Val Asn	
80 85 90	
GAT GAC CTT GCC TAC GGT TTC GCT GTT ACC AAG ATC TCC GGT GGC TCC	144
Asp Asp Leu Ala Tyr Gly Phe Ala Val Thr Lys Ile Ser Gly Gly Ser	
95 100 105	
GAG GCC	150
Glu Ala	

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Asn Asp Asn Pro Ile Ser Asn Thr Asn Ala Val Asn Gly Cys Glu Gly	
1 5 10 15	
Gly Gly Ser Ala Tyr Ala Cys Ser Asn Tyr Ser Pro Trp Ala Val Asn	
20 25 30	
Asp Asp Leu Ala Tyr Gly Phe Ala Val Thr Lys Ile Ser Gly Gly Ser	
35 40 45	

Glu Ala
50

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GTC AAT CAG CCC ATC CGA ACG TGT AGT GCC AAC GAC TCG CCC TTG TCC	48	
Val Asn Gln Pro Ile Arg Thr Cys Ser Ala Asn Asp Ser Pro Leu Ser		
55	60	65

GAC CCA AAT ACC CCA AGT GGC TGT GAC GGT AGC GCC TTC ACT TGT	96	
Asp Pro Asn Thr Pro Ser Gly Cys Asp Gly Gly Ser Ala Phe Thr Cys		
70	75	80

TCC AAC AAC TCC CCG TGG GCA GTC GAT GAC CAG ACA GCT TAT GGC TTT	144	
Ser Asn Asn Ser Pro Trp Ala Val Asp Asp Gln Thr Ala Tyr Gly Phe		
85	90	95

GCG GCA ACA GCC ATC AGT GGC CAG TCC GAG AGC AGC	180	
Ala Ala Thr Ala Ile Ser Gly Gln Ser Glu Ser Ser		
100	105	110

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Val Asn Gln Pro Ile Arg Thr Cys Ser Ala Asn Asp Ser Pro Leu Ser			
1	5	10	15

Asp Pro Asn Thr Pro Ser Gly Cys Asp Gly Gly Ser Ala Phe Thr Cys		
20	25	30

Ser Asn Asn Ser Pro Trp Ala Val Asp Asp Gln Thr Ala Tyr Gly Phe		
35	40	45

Ala Ala Thr Ala Ile Ser Gly Gln Ser Glu Ser Ser
50 55 60

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACC TGC GAC AAG AAG GAC AAC CCC ATC TCT GAT GCC AAC GCC AAG AGC 48
Thr Cys Asp Lys Lys Asp Asn Pro Ile Ser Asp Ala Asn Ala Lys Ser
65 70 75

GGC TGT GAT GGC GGT TCT GCT TTC GCC TGC ACC AAC TAC TCT CCC TTC 96
Gly Cys Asp Gly Gly Ser Ala Phe Ala Cys Thr Asn Tyr Ser Pro Phe
80 85 90

GCC GTC AAC GAC AAC CTC GCC TAC GGT TTC GCT GCC ACC AAG CTT GCT 144
Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Thr Lys Leu Ala
95 100 105

GGA GGC TCC GAG GCT 159
Gly Gly Ser Glu Ala
110

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Thr Cys Asp Lys Lys Asp Asn Pro Ile Ser Asp Ala Asn Ala Lys Ser
1 5 10 15

Gly Cys Asp Gly Gly Ser Ala Phe Ala Cys Thr Asn Tyr Ser Pro Phe
20 25 30

Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Thr Lys Leu Ala
35 40 45

Gly Gly Ser Glu Ala
50

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACC TGC TAC GCC AAT GAC CAG CGC ATC GCC GAC CGC AGC ACC AAG TCC
Thr Cys Tyr Ala Asn Asp Gln Arg Ile Ala Asp Arg Ser Thr Lys Ser
55 60 65

48

GGC TGC GAC GGC GGC TCG GCC TAC TCC TGT TCT
Gly Cys Asp Gly Gly Ser Ala Tyr Ser Cys Ser
70 75 80

81

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Thr Cys Tyr Ala Asn Asp Gln Arg Ile Ala Asp Arg Ser Thr Lys Ser
1 5 10 15

Gly Cys Asp Gly Gly Ser Ala Tyr Ser Cys Ser
20 25

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ACC TGT GAC AAG AAG GAC AAC CCC ATC TCA AAC TTG AAC GCT GTC AAC	48		
Thr Cys Asp Lys Lys Asp Asn Pro Ile Ser Asn Leu Asn Ala Val Asn			
30	35	40	
GGT TGT GAG GGT GGT TCT GCC TTC GCC TGC ACC AAC TAC TCT CCT	96		
Gly Cys Glu Gly Gly Ser Ala Phe Ala Cys Thr Asn Tyr Ser Pro			
45	50	55	
TGG GCG GTC AAT GAC AAC CTT GCC TAC GGC TTC GCT GCA ACC AAG CTT	144		
Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Thr Lys Leu			
60	65	70	75
GCC GGT GGC TCC GAG G	160		
Ala Gly Gly Ser Glu			
80			

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Thr Cys Asp Lys Lys Asp Asn Pro Ile Ser Asn Leu Asn Ala Val Asn			
1	5	10	15
Gly Cys Glu Gly Gly Ser Ala Phe Ala Cys Thr Asn Tyr Ser Pro			
20	25	30	
Trp Ala Val Asn Asp Asn Leu Ala Tyr Gly Phe Ala Ala Thr Lys Leu			
35	40	45	
Ala Gly Gly Ser Glu			
50			

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CCA GTA GGC ACC TGC GAC GCC GGC AAC AGC CCC CTC GGC GAC CCC CTG	48
Pro Val Gly Thr Cys Asp Ala Gly Asn Ser Pro Leu Gly Asp Pro Leu	
55 60 65	
GCC AAG TCT GGC TGC GAG GGC GGC CCG TCG TAC ACG TGC GCC AAC TAC	96
Ala Lys Ser Gly Cys Glu Gly Gly Pro Ser Tyr Thr Cys Ala Asn Tyr	
70 75 80 85	
CAG CCG TGG GCG GTC AAC GAC CAG CTG GCC TAC GGC TTC GCG GCC ACG	144
Gln Pro Trp Ala Val Asn Asp Gln Leu Ala Tyr Gly Phe Ala Ala Thr	
90 95 100	
GCC ATC AAC GGC GGC ACC GAG	165
Ala Ile Asn Gly Gly Thr Glu	
105	

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Pro Val Gly Thr Cys Asp Ala Gly Asn Ser Pro Leu Gly Asp Pro Leu	
1 5 10 15	
Ala Lys Ser Gly Cys Glu Gly Gly Pro Ser Tyr Thr Cys Ala Asn Tyr	
20 25 30	
Gln Pro Trp Ala Val Asn Asp Gln Leu Ala Tyr Gly Phe Ala Ala Thr	
35 40 45	
Ala Ile Asn Gly Gly Thr Glu	
50 55	

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Trp Cys Cys Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Trp Cys Cys Xaa Cys Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Xaa Pro Gly Gly Gly Xaa Gly Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Gly Cys Xaa Xaa Arg Xaa Asp Trp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCCCAAGCTT ACNMGNTAYT GGGAYTGYTG YAARMC

36

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTAGTCTAGA TARCANGCRC ARCACC

26

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTAGTCTAGA AANADNCCNA VNCCNCCNCC NGG

33

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTAGTCTAGA NAACCARTCA RWANCKCC

28

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGGAGCTCAC GTCCAAGAGC GGCTGCTCCC GTCCCTCCAG CAGCACCAGC TCTCCGG

57

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CCGGAGAGCT GGTGCTGCTG GAGGGACGGG AGCAGCCGCT CTGGACGTG AGCTCCG

57

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CGGAGCTCAC GTCCAAGAGC GGCTGCTCCC GTAACGACGA CGGCAACTTC CCTGCCG

57

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CGGCAGGGAA GTTGCCGTCG TCGTTACGGG AGCAGCCGCT CTTGGACGTG AGCTCCG

57

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CAACATCACA TCAAGCTCTC C

21

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CCCCATCCTT TAACTATAGC G

21

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GGTCGCCCGG ACTGGCTGTT CCCGTACCCC CTCCAGCAGC ACCAGCTCTC CGG

53

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CGGGAGAGCT GGTGCTGCTG GAGGGGGTAC GGGAACAGCC AGTCCGGGCG ACC

53

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CGGACTACTA GCAGCTGTAA TACG

24

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GACCGGAGAG CTGGTGCTGC TGGAGGGTTT ACGAACACAG CCCGAGATAT TAGTG

55

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CCCCAAGCTT GACTTGGAAC CAATGGTCCA TCC

33

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CCCCAAGCTT CCATCCAAAC ATGCTTAAAA CGCTCG

36

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CACTAATATC TCGGGCTGTG TTCGTAAACC CTCCAGCAGC ACCAGCTCTC CGGTC

55

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGCGTGAAAT GTAAGCGTGA CATA

24

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Thr Arg Tyr Trp Asp Cys Cys Lys Thr Ser Cys Ala Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Gly Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Xaa Thr Arg Xaa Phe Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Xaa Thr Arg Xaa Tyr Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Xaa Thr Arg Xaa Trp Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Trp Cys Cys Xaa Cys
1 5